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STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,265
FILING DATE: 06-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1744
TELEFAX: 201-994-1700
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: protein
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-467-265-17

Query Match
Best Local Similarity 50.1%; Score 721.5; DB 4; Length 199;
Matches 132; Conservative 27; Mismatches 32; Indels 1; Gaps 1;

QY 79 AKISPAWPEWETAVI-DOEFKELKLTDRGKYLVEFFYPDLFTVCPEITIAFGRLBE 137
DB 6 AKIGPAPWPKATVAMPQGFQDISLSEKKGKVVFFYPDLFTVCPEITIAFGRLBE 65
QY 138 FRSINTEVACVDSQFTHLAWINTPROGGIGPRLIPLSLTHQISKDYGVYEDSGH 197
DB 66 FKLMCGVIGASVDHFECHLAWINTPKQGGIGPNNIPILISPKRTIAQDYGVLADEGI 125
QY 198 TLRLGFIITDDKGLIQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGKPPSEITII 257
DB 126 SFRGLFIITDDKGLIQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGKPPSEITII 257
QY 258 PDPAGKIKYEPK 269
DB 186 PDVAKSKYEFSK 197

SUPT 9
Sequence 17, Application US/09407891
Patent No. 6294164
GENERAL INFORMATION:
APPLICANT: NI, Jian
APPLICANT: Yu, Guo-liang
APPLICANT: Gentz, Reiner
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARBILIA, BARN, BAIN, GILFILLAN, CECCHI,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/407,891
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,265
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1744
TELEFAX: 201-994-1700
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS:
MOLECULE TYPE: protein
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-407-891-17

Query Match
Best Local Similarity 50.1%; Score 721.5; DB 4; Length 199;
Matches 132; Conservative 27; Mismatches 32; Indels 1; Gaps 1;

QY 79 AKISPAWPEWETAVI-DOEFKELKLTDRGKYLVEFFYPDLFTVCPEITIAFGRLBE 137
DB 6 AKIGPAPWPKATVAMPQGFQDISLSEKKGKVVFFYPDLFTVCPEITIAFGRLBE 65
QY 138 FRSINTEVACVDSQFTHLAWINTPROGGIGPRLIPLSLTHQISKDYGVYEDSGH 197
DB 66 FKLMCGVIGASVDHFECHLAWINTPKQGGIGPNNIPILISPKRTIAQDYGVLADEGI 125
QY 198 TLRLGFIITDDKGLIQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGKPPSEITII 257
DB 126 SFRGLFIITDDKGLIQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGKPPSEITII 257
QY 258 PDPAGKIKYEPK 269
DB 186 PDVAKSKYEFSK 197

RESULT 10
Sequence 2, Application US/08299162A
Patent No. 5610286
GENERAL INFORMATION:
APPLICANT: Shau, Hungyi
APPLICANT: Golub, Sidney H
TITLE OF INVENTION: Natural Killer Cell Enhancing Factor
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: David J. Oldenkamp
STREET: 2029 Century Park East, Suite 3800
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,162A
FILING DATE: August 31, 1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J
REFERENCE/DOCKET NUMBER: 104-280

Sequence comparison

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TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-788-5000
 TELEFAX: 310-277-1297
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 199 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-299-162A-2

Query Match
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 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

QY 79 AKISPPAPYMEGTAVI-DGEKELKLTIDYRKGYLVFFPPIDFTFVCPTEIARAGDRL 137
 DB 6 AKIHPAPNPKATVMDGQPKDLSIDYRKGYLVFFPPIDFTFVCPTEIARAGDRL 65
 QY 138 FRSLNTEVAVASVDSQFTLAWINTPRGGLGPIRIRPLSDLTHTQISKDYGVYLED 197
 DB 66 FKRLNCOVIGASVDSHCHLAWNTPRKQGLGPMNIPVSDPKRTIAQDYGVYLED 125
 198 TLGLFLIDKGLIRQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGMPSGSET 257
 126 SFKGLFLIDKGLIRQITVNDPCCRSVDETLRLVQAFQYTDKHGEVCPAGMPSGSET 185
 QY 258 PDPAGKLYFDK 269
 DB 186 PDVPRKTEYFSK 197

RESULT 11

US-08-467-265-14
 Sequence 14, Application US/08467265
 Patent No. 5985612

GENERAL INFORMATION:
 APPLICANT: NI, Jian
 APPLICANT: Yu, Guo-Liang
 APPLICANT: Gentz, Reiner
 APPLICANT: Rosen, Craig A.
 TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,265
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 199 amino acids
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLOGY: linear

MOLECULE TYPE: protein
 US-08-467-265-14

Query Match
 Best Local Similarity 49.5%; Score 713.5; DB 2; Length 199;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

QY 79 AKISPPAPYMEGTAVI-DGEKELKLTIDYRKGYLVFFPPIDFTFVCPTEIARAGDRL 137
 DB 6 AKIHPAPNPKATVMDGQPKDLSIDYRKGYLVFFPPIDFTFVCPTEIARAGDRL 65
 QY 138 FRSLNTEVAVASVDSQFTLAWINTPRGGLGPIRIRPLSDLTHTQISKDYGVYLED 197
 DB 66 FKRLNCOVIGASVDSHCHLAWNTPRKQGLGPMNIPVSDPKRTIAQDYGVYLED 125
 198 TLGLFLIDKGLIRQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGMPSGSET 257
 126 SFKGLFLIDKGLIRQITVNDPCCRSVDETLRLVQAFQYTDKHGEVCPAGMPSGSET 185
 QY 258 PDPAGKLYFDK 269
 DB 186 PDVPRKTEYFSK 197

RESULT 12

US-08-467-265-14
 Sequence 14, Application US/08467265
 Patent No. 6255079

GENERAL INFORMATION:
 APPLICANT: NI, Jian
 APPLICANT: Yu, Guo-Liang
 APPLICANT: Gentz, Reiner
 APPLICANT: Rosen, Craig A.
 TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,265
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 199 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-08-467-265-14

Query Match
 Best Local Similarity 49.5%; Score 713.5; DB 4; Length 199;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

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OM protein - protein search, using sw model

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(without alignments)
531.574 Million cell updates/sec

Title: US-09-911-346-2

Perfect score: 1441

Sequence: 1 MEALPLLAATTPDHGRRL.....GSEIIIPDPACKLKFDKLN 271

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents-AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1441	100.0	271	2	US-08-467-265-2
2	1441	100.0	271	4	US-08-467-265-2
3	1441	100.0	271	4	US-09-407-891-2
4	740	51.4	198	2	US-08-467-265-15
5	740	51.4	198	4	US-08-467-265-15
6	740	51.4	198	4	US-09-407-891-15
7	721.5	50.1	199	2	US-08-467-265-17
8	721.5	50.1	199	4	US-08-467-265-17
9	721.5	50.1	199	4	US-09-407-891-17
10	713.5	49.5	199	1	US-08-299-162A-2
11	713.5	49.5	199	2	US-08-467-265-14
12	713.5	49.5	199	4	US-08-467-265-14
13	713.5	49.5	199	4	US-09-407-891-14
14	689	47.8	257	2	US-08-467-265-16
15	689	47.8	257	4	US-08-467-265-16
16	689	47.8	257	4	US-09-407-891-16
17	683	47.4	199	1	US-08-602-262-2
18	683	47.4	199	3	US-09-004-716-2
19	619	43.0	178	1	US-08-299-162A-4
20	587	40.7	199	4	US-09-183-861-24
21	587	40.7	199	4	US-09-022-765-24
22	586	40.7	206	4	US-09-183-861-26
23	586	40.7	206	4	US-09-022-765-26
24	462	32.1	202	4	US-09-556-877-92
25	462	32.1	202	4	US-09-620-412C-92
26	457	31.7	195	4	US-09-556-877-65
27	457	31.7	195	4	US-09-620-412C-65

28	457	31.7	196	4	US-09-556-877-294	Sequence 294, App
29	457	31.7	196	4	US-09-620-412C-294	Sequence 294, App
30	386.5	26.8	351	1	US-08-415-751-17	Sequence 17, Appl
31	385.5	26.8	201	1	US-08-415-751-2	Sequence 2, Appl
32	290	20.1	196	4	US-09-134-001C-4601	Sequence 4601, Ap
33	170.5	11.8	235	4	US-08-862-540-2	Sequence 2, Appl
34	170.5	11.8	235	4	US-09-633-043-2	Sequence 2, Appl
35	168	11.7	350	1	US-08-415-751-15	Sequence 15, Appl
36	167.5	11.6	235	4	US-08-862-540-9	Sequence 9, Appl
37	167.5	11.6	235	4	US-09-633-043-9	Sequence 9, Appl
38	137.5	9.5	223	4	US-09-411-578-3	Sequence 3, Appl
39	136.5	9.5	157	4	US-09-134-001C-4714	Sequence 4714, Ap
40	106	7.4	28	1	US-07-787-148C-3	Sequence 3, Appl
41	103.5	7.2	214	4	US-08-959-004-1	Sequence 1, Appl
42	100.5	7.0	144	4	US-08-961-083-44	Sequence 44, Appl
43	96.5	6.7	189	4	US-08-959-004-8	Sequence 8, Appl
44	89.5	6.2	168	4	US-09-134-001C-3764	Sequence 3764, Ap
45	84	5.8	2037	4	US-09-306-998-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-467-265-2
; Sequence 2, Application US/08467265
; Patent No. 5985612
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,265
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-467-265-2

Query Match 100.0% Score 1441: DB 2: Length 271:
Best Local Similarity 100.0% Pred. No. 2.5e-15;
Matches 271: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 MEALPLLAATTPDHGRRLLLPLFLPAGAVGMEERPRTRRECHFYAGGY 60
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DB 1 MEALPLLAATTPDHGRRLLLPLFLPAGAVGMEERPRTRRECHFYAGGY 60
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QY 61 PGEASRVSVADHSHLSKAKISKSPAPYWGTAVIDGEFELKLTIDYRGKYLVEFFYPLDF 120
DB 61 PGEASRVSVADHSHLSKAKISKSPAPYWGTAVIDGEFELKLTIDYRGKYLVEFFYPLDF 120
QY 121 TFCVCTEIIAFGDRLEEFERSINTEVAVCSVDSQFTHLAINTPRRGGIGPIRIPILSDL 180
DB 121 TFCVCTEIIAFGDRLEEFERSINTEVAVCSVDSQFTHLAINTPRRGGIGPIRIPILSDL 180
QY 181 THQISKDYGVLIEDSGHTRGLFIIDDKGILRQITLNDLPVGRSVDETLRLVOAFQYTDK 240
DB 181 THQISKDYGVLIEDSGHTRGLFIIDDKGILRQITLNDLPVGRSVDETLRLVOAFQYTDK 240
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DB 241 HGEVCPAGKPKGSETIIPDPAGKLYFDPKLN 271

RESULT 2

US-08-467-265-2
Sequence 2, Application US/08467265
Patent No. 6255079
GENERAL INFORMATION:
APPLICANT: NI, Jian
Yu, Guo-Liang
Gentz, Reiner
Rosen, Craig A.
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467, 265
FILING DATE: 06-Jun-1995
CLASSIFICATION: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-467-265-2

Query Match 100.0%; Score 1441; DB 4; Length 271;
Best Local Similarity 100.0%; Pred. No. 2, 5e-157;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MEALPPLAATPPDGRHRRLLPLLLFLPLPAGAVQGMETERRPTREBECHFYAGGOVY 60
QY 61 PGEASRVSVADHSHLSKAKISKSPAPYWGTAVIDGEFELKLTIDYRGKYLVEFFYPLDF 120
DB 61 PGEASRVSVADHSHLSKAKISKSPAPYWGTAVIDGEFELKLTIDYRGKYLVEFFYPLDF 120
QY 121 TFCVCTEIIAFGDRLEEFERSINTEVAVCSVDSQFTHLAINTPRRGGIGPIRIPILSDL 180
DB 121 TFCVCTEIIAFGDRLEEFERSINTEVAVCSVDSQFTHLAINTPRRGGIGPIRIPILSDL 180
QY 181 THQISKDYGVLIEDSGHTRGLFIIDDKGILRQITLNDLPVGRSVDETLRLVOAFQYTDK 240
DB 181 THQISKDYGVLIEDSGHTRGLFIIDDKGILRQITLNDLPVGRSVDETLRLVOAFQYTDK 240
QY 241 HGEVCPAGKPKGSETIIPDPAGKLYFDPKLN 271
DB 241 HGEVCPAGKPKGSETIIPDPAGKLYFDPKLN 271

QY 121 TFCVCTEIIAFGDRLEEFERSINTEVAVCSVDSQFTHLAINTPRRGGIGPIRIPILSDL 180
DB 121 TFCVCTEIIAFGDRLEEFERSINTEVAVCSVDSQFTHLAINTPRRGGIGPIRIPILSDL 180
QY 181 THQISKDYGVLIEDSGHTRGLFIIDDKGILRQITLNDLPVGRSVDETLRLVOAFQYTDK 240
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DB 241 HGEVCPAGKPKGSETIIPDPAGKLYFDPKLN 271

RESULT 3

US-09-407-891-2
Sequence 2, Application US/09407891
Patent No. 6294164
GENERAL INFORMATION:
APPLICANT: NI, Jian
Yu, Guo-Liang
Gentz, Reiner
Rosen, Craig A.
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/407, 891
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467, 265
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-407-891-2

Query Match 100.0%; Score 1441; DB 4; Length 271;
Best Local Similarity 100.0%; Pred. No. 2, 5e-157;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEALPPLAATPPDGRHRRLLPLLLFLPLPAGAVQGMETERRPTREBECHFYAGGOVY 60
DB 1 MEALPPLAATPPDGRHRRLLPLLLFLPLPAGAVQGMETERRPTREBECHFYAGGOVY 60
QY 61 PGEASRVSVADHSHLSKAKISKSPAPYWGTAVIDGEFELKLTIDYRGKYLVEFFYPLDF 120
DB 61 PGEASRVSVADHSHLSKAKISKSPAPYWGTAVIDGEFELKLTIDYRGKYLVEFFYPLDF 120
QY 121 TFCVCTEIIAFGDRLEEFERSINTEVAVCSVDSQFTHLAINTPRRGGIGPIRIPILSDL 180
DB 121 TFCVCTEIIAFGDRLEEFERSINTEVAVCSVDSQFTHLAINTPRRGGIGPIRIPILSDL 180

Db 121 TFVCPTEIIAEGDRLEERSINTEVAVCSVDQFTHLWIMINTPRQSGILGRIPLSDL 180
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 QY 241 HGEVCPAGMKPGSEIIPDPAGKLYFDKLN 271
 Db 241 HGEVCPAGMKPGSEIIPDPAGKLYFDKLN 271

RESULT 4
 US-08-467-265-15
 : Sequence 15, Application US/08467265
 : Patent No. 5985612
 : GENERAL INFORMATION:
 : APPLICANT: NI, JIAN
 : APPLICANT: Yu, Guo-Liang
 : APPLICANT: Gentz, Reiner
 : APPLICANT: Rosen, Craig A.
 : TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 : NUMBER OF SEQUENCES: 17
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 : ADDRESSEE: STUART & OLSTEIN
 : STREET: 6 Becker Farm Road
 : CITY: Roseland
 : STATE: New Jersey
 : COUNTRY: USA
 : ZIP: 07068
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/467,265
 : FILING DATE: 06-JUN-1995
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Ferraro, Gregory D.
 : REGISTRATION NUMBER: 36,134
 : REFERENCE/DOCKET NUMBER: 325800-456
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 201-994-1700
 : TELEFAX: 201-994-1744
 : INFORMATION FOR SEQ ID NO: 15:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 198 amino acids
 : TYPE: amino acid
 : STRANDEDNESS:
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-467-265-15

Query Match 51.4%; Score 740; DB 2; Length 198;
 Best Local Similarity 69.9%; Pred. No. 5.8e-77;
 Matches 135; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

QY 79 AKIKPAPYMGCTAVIOGEFEKLTQYRGKYLVEFFPLDFTVCPEIIAAGDRLEEF 138
 Db 6 ARICKPAPDERATAVDQAEKVLSDKGYVLEFFPLDFTVCPEIIAAGDRLEEF 65
 QY 139 RSINTEVAVCSVDQFTHLWIMINTPRQSGILGRIPLSDLTHQISKQYGVLEDSGHT 198
 Db 66 RKLCEVYLGVSVDQFTHLWIMINTPRQSGILGRIPLSDLTHQISKQYGVLEDSGHT 125
 QY 199 LRGLFIIDDKGILROITLNDLPVGRSVDETLRLVOAFQYTDK HGEVCPAGMKPGSEIIP 258
 Db 126 YRGLFIIDDKGILROITLNDLPVGRSVDETLRLVOAFQYTDK HGEVCPAGMKPGSEIIP 185
 QY 259 DPAGKLYFDKLN 271

Db 186 NVDDSKETFSKHN 198

RESULT 5
 US-08-467-265-15
 : Sequence 15, Application US/08467265
 : Patent No. 6255079
 : GENERAL INFORMATION:
 : APPLICANT: NI, JIAN
 : APPLICANT: Yu, Guo-Liang
 : APPLICANT: Gentz, Reiner
 : APPLICANT: Rosen, Craig A.
 : TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 : NUMBER OF SEQUENCES: 17
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 : ADDRESSEE: STUART & OLSTEIN
 : STREET: 6 Becker Farm Road
 : CITY: Roseland
 : STATE: New Jersey
 : COUNTRY: USA
 : ZIP: 07068
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/467,265
 : FILING DATE: 06-JUN-1995
 : CLASSIFICATION: <unknown>
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Ferraro, Gregory D.
 : REGISTRATION NUMBER: 36,134
 : REFERENCE/DOCKET NUMBER: 325800-456
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 201-994-1700
 : TELEFAX: 201-994-1744
 : INFORMATION FOR SEQ ID NO: 15:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 198 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: <unknown>
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : SEQUENCE DESCRIPTION: SEQ ID NO: 15:
 : US-08-467-265-15

Query Match 51.4%; Score 740; DB 4; Length 198;
 Best Local Similarity 69.9%; Pred. No. 5.8e-77;
 Matches 135; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

QY 79 AKIKPAPYMGCTAVIOGEFEKLTQYRGKYLVEFFPLDFTVCPEIIAAGDRLEEF 138
 Db 6 ARICKPAPDERATAVDQAEKVLSDKGYVLEFFPLDFTVCPEIIAAGDRLEEF 65
 QY 139 RSINTEVAVCSVDQFTHLWIMINTPRQSGILGRIPLSDLTHQISKQYGVLEDSGHT 198
 Db 66 RKLCEVYLGVSVDQFTHLWIMINTPRQSGILGRIPLSDLTHQISKQYGVLEDSGHT 125
 QY 199 LRGLFIIDDKGILROITLNDLPVGRSVDETLRLVOAFQYTDK HGEVCPAGMKPGSEIIP 258
 Db 126 YRGLFIIDDKGILROITLNDLPVGRSVDETLRLVOAFQYTDK HGEVCPAGMKPGSEIIP 185
 QY 259 DPAGKLYFDKLN 271
 Db 186 NVDDSKETFSKHN 198

RESULT 6
 US-09-407-891-15
 : Sequence 15, Application US/09407891

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; Patent No. 6294164
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Yu, Guo-liang
; APPLICANT: Gentz, Reiner
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/407,891
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,265
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-456
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-407-891-15

Query Match          51.4%; Score 740; DB 4; Length 198;
Best Local Similarity 69.9%; Pred. No. 5.8e-77;
Matches 135; Conservative 25; Mismatches 33; Indels 0; Gaps 0;
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; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,265
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-456
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-467-265-17

Query Match          50.1%; Score 721.5; DB 2; Length 199;
Best Local Similarity 68.8%; Pred. No. 7.8e-75;
Matches 132; Conservative 27; Mismatches 32; Indels 1; Gaps 1;
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1      RESULT 9
2      US-09-407-891-17
3      ; Sequence 17, Application US/09407891
4      ; Patent No 6294164
5      ;
6      ; GENERAL INFORMATION:
7      ;
8      ; APPLICANT: NI, Jlan
9      ; APPLICANT: Yu, Guo-Liang
10     ; APPLICANT: Gentz, Reiner
11     ; APPLICANT: Rosen, Craig A.
12     ; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
13     ; NUMBER OF SEQUENCES: 17
14     ;
15     ; CORRESPONDENCE ADDRESS:
16     ;
17     ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
18     ; ADDRESSEE: STUART & OLSTEIN
19     ; STREET: 6 Becker Farm Road
20     ; CITY: Roseland
21     ; STATE: New Jersey
22     ; COUNTRY: USA
23     ; ZIP: 07068
24     ;
25     ; COMPUTER READABLE FORM:
26     ;
27     ; MEDIUM TYPE: Floppy disk
28     ;
29     ; COMPUTER: IBM PC compatible
30     ;
31     ; OPERATING SYSTEM: PC-DOS/MS-DOS

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RESULT 10
 US-08-299-162A-2
 : Sequence 2, Application US/08299162A
 : Patent No. 5610286
 : GENERAL INFORMATION:
 :
 : APPLICANT: Shau, Hungyi
 :
 : APPLICANT: Golub, Sidney H
 :
 : TITLE OF INVENTION: Natural Killer Cell Enhancing Factor
 :
 : NUMBER OF SEQUENCES: 4
 :
 : CORRESPONDENCE ADDRESS:
 :
 : ADDRESSEE: David J. Oldenkamp
 :
 : STREET: 2029 Century Park East, Suite 3800
 :
 : CITY: Los Angeles
 :
 : STATE: CA
 :
 : COUNTRY: USA
 :
 : ZIP: 90067
 :
 : COMPUTER READABLE FORM:
 :
 : MEDIUM TYPE: Floppy disk
 :
 : COMPUTER: IBM PC compatible
 :
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 :
 : SOFTWARE: Patentln Release #1.0, Version #1.25
 :
 : CURRENT APPLICATION DATA:
 :
 : APPLICATION NUMBER: US/08/299.162A
 :
 : FILING DATE: August 31, 1994
 :
 : CLASSIFICATION: 536
 :
 : ATTORNEY/AGENT INFORMATION:
 :
 : NAME: Oldenkamp, David J
 :
 : REFERENCE/DOCKET NUMBER: 104-280

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-788-5000
TELEFAX: 310-277-1297
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-299-162A-2

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Query Match
Best Local Similarity 49.5%; Score 713.5; DB 1; Length 199;
Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

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QY 79 AKIKPAPYMEGTAVI-DGEFEKELADYRGKYLVFFFPYPLDFTFVCPTEIIAAGDRLEE 137
Db 6 AKIGHPAPNFKATVAMPDGGCFKDISLDYKGYVFFFPYPLDFTFVCPTEIIASDRAEE 65
QY 138 FRSINTEVAVASVDSQFTHLAWINTPRQGLGPIRIPLSDLTHQISKDYGVLDSGH 197
Db 66 FKKLNCQVIGASVDSHFCHLAWMTPKQGLGPMNIPLVSDPKRTTAODYGLKADEGI 125
QY 198 TLGSLFIIDDKGILRQITLNDLPYGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETII 257
Db 126 SFRLGFIIDDKGILRQITVNDPCCRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSDTIK 185
QY 258 PDPAGKAKYFDK 269
Db 186 PDVPKTKYFYSK 197

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```

RESULT 11
US-08-467-265-14
Sequence 14, Application US/08467265
Patent No. 5985612
GENERAL INFORMATION:
APPLICANT: NI, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,265
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

```

```

MOLECULE TYPE: protein
US-08-467-265-14

```

```

Query Match
Best Local Similarity 49.5%; Score 713.5; DB 2; Length 199;
Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

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QY 79 AKIKPAPYMEGTAVI-DGEFEKELADYRGKYLVFFFPYPLDFTFVCPTEIIAAGDRLEE 137
Db 6 AKIGHPAPNFKATVAMPDGGCFKDISLDYKGYVFFFPYPLDFTFVCPTEIIASDRAEE 65
QY 138 FRSINTEVAVASVDSQFTHLAWINTPRQGLGPIRIPLSDLTHQISKDYGVLDSGH 197
Db 66 FKKLNCQVIGASVDSHFCHLAWMTPKQGLGPMNIPLVSDPKRTTAODYGLKADEGI 125
QY 198 TLGSLFIIDDKGILRQITLNDLPYGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETII 257
Db 126 SFRLGFIIDDKGILRQITVNDPCCRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSDTIK 185
QY 258 PDPAGKAKYFDK 269
Db 186 PDVPKTKYFYSK 197

```

```

RESULT 12
US-08-467-265-14
Sequence 14, Application US/08467265
Patent No. 6255079
GENERAL INFORMATION:
APPLICANT: NI, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,265
FILING DATE: 06-JUN-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-08-467-265-14

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```

Query Match
Best Local Similarity 49.5%; Score 713.5; DB 4; Length 199;
Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

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0Y      79 AKISKPAWMEGTAVI -DGEKEKELNDYRKRYLVFFFYFLDTFVCPTEIIAAGDRLEE 137
         ||| |::||| :|||::| ::|:|||::|||||::|::|::| |||
Db       6 AKIHAPAFNEATVAVMPPGQFKDISLDKYKKYVVFFEFPDLDFEVCPTETIAFSDAEE 65
0Y     138 FRSINTEVEVASVSOFTHLAWINTPRROGLGPRIPLLSDDLTHOISKRXYGYVLDSCH 197
        |:| :|: ||| | |||::|::|::|::|::|::|::|::|::|::|::| 
Db       66 FKRLNCQVTIGASVSHFCHELANVMTPKKGSGLFPMNIPLYSDPKRTTAODITGVLRKADEGI 125
0Y     198 TLRGLEFIIDXGDILRQLTILLDPYGRSVDELTRLVQAFOYTDKHGEACPAMWGSETII 257
        : |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::| 
Db    126 SERGLEFITDXDGILRQLTVINDRPCCRSVDFTLLRVQAFQTCDKHGEIVCAPGMWRGSSTIK 185
0Y     258 PDPAKGLKTYPDK 269
        ||| |::| | 
Db    186 PDVPKTKYEFGSK 197

RESULT   13
US-09-407-891-14
; Sequence 14, Application US/09407891
; Patent No. 6294164
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-liang
; APPLICANT: Gentz, Reiner
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
; NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CARELLA, BYRNIE BAIN, GILFILLAN, CECCHI,
ADDRESSER: STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/407,891
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,265
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEX: 201-994-1744
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-407-891-14
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Query Match	49.5%	Score 713.5	DB 4:	Length 199
Best Local Similarity	68.8%	Pred. No. 6.5e-74		
Matches 132:	Conservative 25;	Mismatches 34;	Indels 1;	Gaps 1;
QY	79	AKISRPAPYECSTAVI-DGEFKELKLDIRGKLYVFFYPPLDFTVCPTETIAAGDRLKE	137	
Db	6	AKIGHAPAFKRTAAMPDQGFIDSLSDKGVYVFFPPLDFTVCPTETIAAFEDRAEE	65	
QY	138	FRSINTEVYACVDSQETHLAININPRROGGCGIPRIPLISDITLQISKDYGVYLEDSDGH	197	

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Db      66 EKRLNCQYIGASVSDSHFCHLAWMTPKKGGGLGPMNIPLVSDPKRTIADQYGVLKADEGI 1255
Oy     198 TLRGILFIIDDDGILRQITLANDLPGRSVDETFLRVQAFOYTDRKGCEVPAGMKPGSETII 257
Db    126 SRRGILFITDGDGILRQITAVNDPPCCRSVDETLRVAOFOTFDKHGECPAGMKGPSDTIK 105
Oy    258 PDPAKGLKYFKDK 269
Db   186 PDPVKTKKEYFSK 197

RESULT 14
US-08-467-265-16
; Sequence 16, Application US/08467265
; Patent No. 5985612
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-liang
; APPLICANT: Gentz, Reinher
; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNIE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,265
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-265-16
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[illegible]

DB 246 TASKEYFEKVH 256

RESULT 15

US-08-467-265-16

Sequence 16, Application US/08467265

Patent No. 6255079

GENERAL INFORMATION:

APPLICANT: NI, Jian

Yu, Guo-Liang

Gentz, Reiner

Rosen, Craig A.

TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS: 17

ADDRESS: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

STUART & OLSTEIN

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: New Jersey

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,265

FILING DATE: 06-Jun-1995

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Ferraro, Gregory D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-456

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-08-467-265-16

Query Match 47.88; Score 689; DB 4; Length 257;
Best Local Similarity 64.48; Pred. No. 6.3e-71;
Matches 123; Conservative 32; Mismatches 36; Indels 0; Gaps 0;

QY 81 ISKPAPYMEGTAVIDGCEKELKLTDRGKYLFFVPLDFTFVCPTELIARGLRLEPFRS 140
DB 66 VTQHAPYFKGTAAVNGEKEKELSLDDEKGYLVLFYPLDFTFVCPTELIARGLRLEPFRS 125
QY 141 INTEVAVACVSQDFTLAWINTPRGGGLGPIRIPLSDLTHQISKDYGVYLEDGHTLR 200
DB 126 VNCEVAVASVDSHRSFLAWITPRKNGLGSHMITLLSDITKQISRDYGVYLEDGHTLR 185
QY 201 GLFTIIDKGLRQTLNDLPGRSVDETLLRYQAFQYTDKHGEVCPAGWKPGSETITPDP 260
DB 186 GLFTIIDKGLRQTLNDLPGRSVDETLLRYQAFQYTDKHGEVCPAGWKPGSETITPDP 245
QY 261 AGKLKYPDKLN 271
DB 246 TASKEYFEKVH 256

Search completed: January 17, 2003, 19:19:59
Job time: 17 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:18:27 : Search time 13 Seconds
(without alignments)
414.391 Million cell updates/sec

Title: US-09-911-346-2
Perfect score: 1441
Sequence: 1 MEALPLLATPTDGHGHRRL.....GSETIIPDPAKLYFDKLN 271

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database: Published.Applications_AA:*

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4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1441	100.0	271	10	US-09-911-346-2
2	750.5	52.1	233	10	US-09-925-301-973
3	740	51.4	198	10	US-09-911-346-15
4	721.5	50.1	199	10	US-09-911-346-17
5	713.5	49.5	199	10	US-09-911-346-14
6	703	48.8	224	10	US-09-925-300-1537
7	689	47.8	257	10	US-09-911-346-16
8	598	41.5	925	9	US-09-991-496-128
9	598	41.5	925	9	US-09-991-496-127
10	598	41.5	982	9	US-09-991-496-95
11	598	41.5	982	10	US-09-874-923-95
12	598	41.5	1427	9	US-09-991-496-97
13	598	41.5	1427	10	US-09-874-923-97
14	598	41.5	1641	9	US-09-991-496-96
15	598	41.5	1641	10	US-09-874-923-96
16	591	41.0	446	9	US-10-025-380-1121
17	591	41.0	446	10	US-09-922-217-1121
18	591	41.0	1464	9	US-10-012-896-1008
19	587	40.7	199	9	US-09-991-496-24

20	587	40.7	199	10	US-09-874-923-24	Sequence 24, Appl
21	586	40.7	206	9	US-09-991-496-26	Sequence 26, Appl
22	586	40.7	206	10	US-09-874-923-26	Sequence 7, Appl
23	478	33.2	114	10	US-09-819-505-7	Sequence 8, Appl
24	474	32.9	114	10	US-09-819-505-8	Sequence 92, Appl
25	462	32.1	202	10	US-09-841-133-92	Sequence 65, Appl
26	457	31.7	195	10	US-09-841-133-65	Sequence 294, App
27	457	31.7	196	10	US-09-841-133-294	Sequence 101, App
28	455	31.6	195	12	US-10-007-693-101	Sequence 76, Appl
29	444	30.8	196	12	US-10-007-693-76	Sequence 11459, A
30	425	29.5	114	10	US-09-819-505-6	Sequence 10881, A
31	403	28.0	198	10	US-09-815-242-11459	Sequence 13714, A
32	358	24.8	187	10	US-09-815-242-10591	Sequence 11776, A
33	333	23.1	187	10	US-09-815-242-10081	Sequence 1445, Ap
34	328	22.8	187	10	US-09-815-242-13714	Sequence 12752, A
35	326	22.6	187	10	US-09-815-242-11776	Sequence 13142, A
36	323.5	22.4	126	10	US-09-925-300-1753	Sequence 41230, A
37	314	21.8	126	10	US-09-925-300-1445	Sequence 37, Appl
38	279	19.4	189	10	US-09-815-242-5318	Sequence 4, Appl
39	279	19.4	189	10	US-09-815-242-13409	
40	279	19.4	189	10	US-09-815-242-12752	
41	279	19.4	189	10	US-09-815-242-13142	
42	201	13.9	50	10	US-09-864-761-41230	
43	179.5	12.5	224	10	US-09-728-914-37	
44	172	11.9	224	10	US-09-819-505-4	
45	171.5	11.9	224	9	US-09-981-553-4	

ALIGNMENTS

RESULT 1
US-09-911-346-2
Sequence 2, Application US/09911346
Patent No. US20020106323A1
GENERAL INFORMATION:
APPLICANT: NI, Jian
Yu, Guo-Liang
Gentz, Reiner
Rosen, Craig A.
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/911,346
FILING DATE: 24-Jul-2001
CLASSIFICATION: <Unknown>
Prior Application DATA:
APPLICATION NUMBER: US 08/467,265
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2
US-09-911-346-2

Query Match 100.0%; Score 1441; DB 10; Length 271;
Best Local Similarity 100.0%; Pred. No. 5,7e-139;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEALPLAATPDGRRHRLRLPLLEFLPAGAVQWTEPERTRRECHFYAGGQVY 60
DB 1 MEALPLAATPDGRRHRLRLPLLEFLPAGAVQWTEPERTRRECHFYAGGQVY 60
QY 61 PGASRSVADHSLHLSKAKISKPAPYWEQAVDGEKELTDYRKYLVFFPYLDF 120
DB 61 PGASRSVADHSLHLSKAKISKPAPYWEQAVDGEKELTDYRKYLVFFPYLDF 120
QY 121 TVCPTEIIAFGRLEERSINTEVAVCSVDQFTHLAMINTPRROGLGPIRIPLSDL 180
DB 121 TVCPTEIIAFGRLEERSINTEVAVCSVDQFTHLAMINTPRROGLGPIRIPLSDL 180
QY 181 THQISKQYGVLEDSGHTLKGFLITIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDK 240
DB 181 THQISKQYGVLEDSGHTLKGFLITIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDK 240
QY 241 HGEVCPAGMKPGSETIIPDPAGKLYFDKLN 271
DB 241 HGEVCPAGMKPGSETIIPDPAGKLYFDKLN 271

RESULT 2

US-09-925-301-973
Sequence 973, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 973
LENGTH: 233
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (3)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-973

Query Match 52.1%; Score 750.5; DB 10; Length 233;
Best Local Similarity 67.1%; Pred. No. 7,9e-69;
Matches 139; Conservative 27; Mismatches 40; Indels 1; Gaps 1;

QY 64 ASRVAVADHSLHLSKAKISKPAPYWEQAVI-DGEKELTDYRKYLVFFPYLDF 122
DB 25 ANCVGADAKMKSSGNKIKHPANFRKATVMPDQCKDLSYKGYVFFPYLDF 84
QY 123 VCPTEIIAFGRLEERSINTEVAVCSVDQFTHLAMINTPRROGLGPIRIPLSDL 182
DB 85 VCPTEIIAFGRLEERSINTEVAVCSVDQFTHLAMINTPRROGLGPIRIPLSDL 182
QY 183 THQISKQYGVLEDSGHTLKGFLITIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDK 242
DB 145 THQISKQYGVLEDSGHTLKGFLITIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDK 242
QY 243 HGEVCPAGMKPGSETIIPDPAGKLYFDK 269

DB 205 EVCPAGMKPGSDTIKPDVOKSEYFSK 231

RESULT 3

US-09-911-346-15
Sequence 15, Application US/09911346
Patent No. US20020106323A1
GENERAL INFORMATION:
APPLICANT: NI, Jian
Yu, Guo-Liang
Genetz, Reiner
Rosen, Craig A.
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STUART & OLSTEIN
STREET: 6 Becker Farm Road
City: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/911,346
FILING DATE: 24-Jul-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,265
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-911-346-15

Query Match 51.4%; Score 740; DB 10; Length 198;
Best Local Similarity 69.9%; Pred. No. 7,3e-68;
Matches 135; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

QY 79 AKISKPAPYWEQAVDGEKELTDYRKYLVFFPYLDFVCPTEIIAFGRLEEF 138
DB 6 ARGRKAPRPFKATVAVDAGFKYKLSYKGYVFFPYLDFVCPTEIIAFGRLEEF 65
QY 139 RSTNEVAVCSVDQFTHLAMINTPRROGLGPIRIPLSDLTHQISKQYGVLEDSGHT 198
DB 66 RKGCEVAGVSDQFTHLAMINTPRROGLGPIRIPLSDLTHQISKQYGVLEDSGHT 198
QY 199 LRGFLITIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETIIP 258
DB 126 YRGFLITIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETIIP 258
QY 259 DPAGKLYFDKLN 271
DB 186 NVDDSKSEYFSKH 198


```
RESULT 4
US-09-911-346-17
; Sequence 17, Application US/09911346
; Patent No. US20020106323A1
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; Yu, Guo-Liang
; Gentz, Reiner
; Rosen, Craig A.
; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/911,346
; FILING DATE: 24-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,265
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-456
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-911-346-17

Query Match          50.1%; Score 721.5; DB 10; Length 199;
Best Local Similarity 68.8%; Pred. No. 5,6e-66;
Matches 132; Conservative 27; Mismatches 32; Indels 1; Gaps 1;

QY 79 AKISKAPAYMEGTAVI-DGEFEKELKLDYRGKYLVEFFYPLDFTFVCPTEIIAFGBLLE 137
   ||| ||| :: ||| :: ||| :: ||| :: ||| :: ||| :: ||| :: ||| :: |||
Db 6 AKIGYAPAPNKATAVMPDGGFKDISLSEYKGVVFEFFYPLDFTFVCPTEIIAFSDRAE 65
   : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 138 FRSINTEVAVCSVDQSOTFLHAWINTPRROGGLPIRIPILSDLTHTQISKDYGYLSDSGH 197
   : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 66 FKKLNQVIGASVDSHCHLAWINTPRKOGGLPMNIPILSDPKRTIADQYGVLLKADDEGI 125
   : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 198 TLKGLFTIDDKGILRQTLTNDLPLVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETII 257
   : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 126 SFGGLFTIIDDKGILRQTLTNDLPLVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSDTIK 185
   : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 258 PDPAGRLKYFDK 269
   || : ||| :
Db 186 PDVAKSKREYFSK 197

RESULT 5
US-09-911-346-14
; Sequence 14, Application US/09911346
; Patent No. US20020106323A1
```

```
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; Yu, Guo-Liang
; Gentz, Reiner
; Rosen, Craig A.
; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/911,346
; FILING DATE: 24-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,265
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-456
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-911-346-14

Query Match          49.5%; Score 713.5; DB 10; Length 199;
Best Local Similarity 68.8%; Pred. No. 3.7e-65;
Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

QY 79 AKISKAPAYMEGTAVI-DGEFEKELKLDYRGKYLVEFFYPLDFTFVCPTEIIAFGBLLE 137
   ||| ||| :: ||| :: ||| :: ||| :: ||| :: ||| :: ||| :: ||| :: |||
Db 6 AKIGHPAPNKATAVMPDGGFKDISLSDYKGVVFEFFYPLDFTFVCPTEIIAFSDRAE 65
   : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 138 FRSINTEVAVCSVDQSOTFLHAWINTPRROGGLPIRIPILSDLTHTQISKDYGYLSDSGH 197
   : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 66 FKKLNQVIGASVDSHCHLAWINTPRKOGGLPMNIPILSDPKRTIADQYGVLLKADDEGI 125
   : : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 198 TLKGLFTIDDKGILRQTLTNDLPLVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETII 257
   : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 126 SFGGLFTIIDDKGILRQTLTNDLPLVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSDTIK 185
   : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 258 PDPAGRLKYFDK 269
   || : ||| :
Db 186 PDVAKTKREYFSK 197

RESULT 6
US-09-925-300-1537
; Sequence 1537, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; Applicant: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
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Db 126 LEESGVAAYRCLFIIDDPGMLRQITTVNDMPVGRSVEEYLRLLLEAFQVEKHGEVCPANMK 185

QY 251 PGSEFIIDDPAGKLLK-YFDK 269

Db 186 KGAPFMKPEPNASVEGYFSK 205

RESULT 9

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US-09-991-496-127
: Sequence 127, Application US/09991496
: Patent No. US20020169285A1
:
: GENERAL INFORMATION:
: APPLICANT: Reed, Steven G.
: APPLICANT: Campos-Neto, Antonio
: APPLICANT: Webb, John R.
: APPLICANT: Dillon, David C.
: APPLICANT: Skelky, Yasir A.W.
: APPLICANT: Bhatia, Ajay
: APPLICANT: Coler, Rhea
: APPLICANT: Probst, Peter
: APPLICANT: Brannon, Mark
: TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
: TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
: FILE REFERENCE: 210121.420C9
: CURRENT APPLICATION NUMBER: US/09/991.496
: CURRENT FILING DATE: 2001-11-20
: NUMBER OF SEQ ID NOS: 137
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 127
: LENGTH: 955
: TYPE: prf
: ORGANISM: Leishmania major
: US-09-991-496-127

```

Query Match	41.5%	Score 598	DB 9	Length 955
Best Local Similarity	54.0%	Pred. No. 1.8e-52		
Matches 108, Conservative	39	Mismatches 51	Indels 2	Gaps 2

RESULT 10

US-09-991-496--95
Sequence 95, Application US/09991496
Patent No. US20020169285A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Netlo, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, David C.
APPLICANT: Skelky, Victor A.W.
APPLICANT: Bhatia, Ajay
APPLICANT: Colier, Rhea
APPLICANT: Probst, Peter
APPLICANT: Brannon, Mark
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.420C9
CURRENT APPLICATION NUMBER: US/09/991,496

```

: CURRENT FILING DATE: 2001-11-20
: NUMBER OF SEQ. ID NOS: 137
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ. ID NO 95
: LENGTH: 982
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
: OTHER INFORMATION: Leishmania antigens
: US-09-991-496-95

```

Query Match	41.5%	Score 598	DB 9	Length 982
Best Local Similarity	54.0%	Pred. No. 1.9e-52		
Matches 108; Conservative	39;	Mismatches 51;	Indels 2;	Gaps 2

RESULT 11

```

US-09-874-923-95
Sequence 95, Application us/09874923
Patent No. US20020081320A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Bhalla, Ajay
APPLICANT: Coler, Rhea
APPLICANT: Probst, Peter
APPLICANT: Brannon, Mark
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.42008
CURRENT APPLICATION NUMBER: US/09/874,923
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 95
LENGTH: 982
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
US-09-874-923-95

```

Query Match	41.5%	Score 598	DB 10	Length 982
Best Local Similarity	54.0%	Pred. No. 1.9e-52		
Matches 108; Conservative	39;	Mismatches 51;	Indels 2;	Gaps 2

OY 72 HSLHLSAKISKPPAPYNEGTAVI-DGFEKRLKTLDYRGKVLVEFPVLPDFTVCPEEIIA 130
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 6 HHMSGNKAINSPAPSEEEVALMNGSFKKISLSSYKGWVLFEPYPLDFTVCPEEIIA 65
OY 131 FGDRIEPRRSINTVEAVACSVDOSQTHAMINTNRROGGACPIRIPLLSLDTMQISKDVY 190
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |

Db 66 FSDSVSRFNLNCEVLACSIDSEYAHQWTLQDRKKGGLGTMAIPMLADTKSIARSGV 125
 QY 191 YLEDSGHTLRGLFIIDDKILRQITLNDLPVGRSVDETLRLVOAFQYTDKHGEVCPAGMK 250
 Db 126 LBSQGVAYRGLFIIDPHGLRQITVNDMPVGRSVDEVLRLLEAFQVEKHGEVCPANMK 185
 QY 251 PGSETIIPDPACKLK-YFDK 269
 Db 186 KGAPTMKPEPNASVEGYFSK 205

RESULT 12 US-09-991-496-97

; Sequence 97, Application US/09991496
 ; Patent No. US20020169285A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Campos-Neto, Antonio
 ; APPLICANT: Webb, John R.
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Skelky, Yasir A.W.
 ; APPLICANT: Bhatia, Ajay
 ; APPLICANT: Coler, Rhea
 ; APPLICANT: Probst, Peter
 ; APPLICANT: Brannon, Mark
 ; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
 ; FILE REFERENCE: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
 ; CURRENT APPLICATION NUMBER: US/09/991,496
 ; CURRENT FILING DATE: 2001-11-20
 ; NUMBER OF SEQ ID NOS: 137
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 97
 ; LENGTH: 1427
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
 ; US-09-991-496-97

Query Match 41.5%; Score 598; DB 9; Length 1427;
 Best Local Similarity 54.0%; Pred. No. 3,1e-52;
 Matches 108; Conservative 39; Mismatches 51; Indels 2; Gaps 2;

QY 72 HSLHLSKAKISKRPAYWEGTAVI-DGEFKELKLDYRGKYLVEFFYPDLDTFVCPTETIA 130
 Db 6 HMSCGNKAKINSPAPSEFEVALMPNGSFKKISLSYKGMVLFEPDLDTFVCPTETIA 65
 QY 131 FGDRLEEFSSINTEVAVCSVDSQFTHLANINPRROGGLGPIRIPILSLDTHQISKDYG 190
 Db 66 FSDSVSRFNLNCEVLACSIDSEYAHQWTLQDRKKGGLGTMAIPMLADTKSIARSGV 125
 QY 191 YLEDSGHTLRGLFIIDDKILRQITLNDLPVGRSVDETLRLVOAFQYTDKHGEVCPAGMK 250
 Db 126 LBSQGVAYRGLFIIDPHGLRQITVNDMPVGRSVDEVLRLLEAFQVEKHGEVCPANMK 185
 QY 251 PGSETIIPDPACKLK-YFDK 269
 Db 186 KGAPTMKPEPNASVEGYFSK 205

RESULT 13 US-09-874-923-97

; Sequence 97, Application US/09874923
 ; Patent No. US20020081320A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Campos-Neto, Antonio
 ; APPLICANT: Webb, John R.
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Skelky, Yasir A.W.
 ; APPLICANT: Bhatia, Ajay

; APPLICANT: Coler, Rhea
 ; APPLICANT: Probst, Peter
 ; APPLICANT: Brannon, Mark
 ; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
 ; FILE REFERENCE: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
 ; CURRENT APPLICATION NUMBER: US/09/874,923
 ; CURRENT FILING DATE: 2001-06-04
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 97
 ; LENGTH: 1427
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
 ; US-09-874-923-97

Query Match 41.5%; Score 598; DB 10; Length 1427;
 Best Local Similarity 54.0%; Pred. No. 3,1e-52;
 Matches 108; Conservative 39; Mismatches 51; Indels 2; Gaps 2;

QY 72 HSLHLSKAKISKRPAYWEGTAVI-DGEFKELKLDYRGKYLVEFFYPDLDTFVCPTETIA 130
 Db 6 HMSCGNKAKINSPAPSEFEVALMPNGSFKKISLSYKGMVLFEPDLDTFVCPTETIA 65
 QY 131 FGDRLEEFSSINTEVAVCSVDSQFTHLANINPRROGGLGPIRIPILSLDTHQISKDYG 190
 Db 66 FSDSVSRFNLNCEVLACSIDSEYAHQWTLQDRKKGGLGTMAIPMLADTKSIARSGV 125
 QY 191 YLEDSGHTLRGLFIIDDKILRQITLNDLPVGRSVDETLRLVOAFQYTDKHGEVCPAGMK 250
 Db 126 LBSQGVAYRGLFIIDPHGLRQITVNDMPVGRSVDEVLRLLEAFQVEKHGEVCPANMK 185
 QY 251 PGSETIIPDPACKLK-YFDK 269
 Db 186 KGAPTMKPEPNASVEGYFSK 205

RESULT 14 US-09-991-496-96

; Sequence 96, Application US/09991496
 ; Patent No. US20020169285A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Campos-Neto, Antonio
 ; APPLICANT: Webb, John R.
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Skelky, Yasir A.W.
 ; APPLICANT: Coler, Rhea
 ; APPLICANT: Probst, Peter
 ; APPLICANT: Brannon, Mark
 ; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
 ; FILE REFERENCE: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
 ; CURRENT APPLICATION NUMBER: US/09/991,496
 ; CURRENT FILING DATE: 2001-11-20
 ; NUMBER OF SEQ ID NOS: 137
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 96
 ; LENGTH: 1641
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
 ; US-09-991-496-96

Query Match 41.5%; Score 598; DB 9; Length 1641;
 Best Local Similarity 54.0%; Pred. No. 3,8e-52;
 Matches 108; Conservative 39; Mismatches 51; Indels 2; Gaps 2;

[illegible]

RESULT 15
US-09-874

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? Sequence 96, Application us/09874923
? Patent No. US20020081320A1
? GENERAL INFORMATION:
? APPLICANT: Reed, Steven G.
? APPLICANT: Campos-Neto, Antonio
? APPLICANT: Webb, John R.
? APPLICANT: Dillon, Davin C.
? APPLICANT: Skeiky, Yasir A.W.
? APPLICANT: Bhatia, Ajay
? APPLICANT: Coler, Rhea
? APPLICANT: Probst, Peter
? APPLICANT: Brannon, Mark
? TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
? TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
? FILE REFERENCE: 210121.42008
? CURRENT APPLICATION NUMBER: US/09/874,923
? CURRENT FILING DATE: 2001-06-04
? NUMBER OF SEQ ID NOS: 122
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 96
? LENGTH: 1641
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
? OTHER INFORMATION: Leishmania antilens
? US-09-874-923-96

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Query Match	41.5%	Score 598	DB 10	Length 1641
Best Local Similarity	54.0%	Pred. No. 3.8e-52		
Matches 108	Conservative 39	Mismatches 51	Indels 2	Gaps 2

QY	72	LSHLHSKSKKPPAPYMGSTAVI-DGEKELKILDYGGKVLVEFYPLDTPPCPEIIA	130
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	6	HHMSGNAKINSPAPSEFEVALMPNGSEKTKISLSTYSGKMWLFYPLDTPPCPEIIA	65
QY	131	FGDRLEEFRRINTEPVACSVSDQFTLHAMINTPRQCGLGPIRIPRLDSTLTHDISKRYG	190
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	66	FSDYSRRNELNCEVLAWSIDSEVAHILQWTLIDDKKGGSLGTMAIRPLADTKTSLARYG	125
QY	191	YLEDSGHTLRGLFIIDDKGILRQTLTLDLPVGRSVDETLRLIYVAFQYTDKHGEVCPAGWK	250
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	126	LEESQGVAYRGLFIIDPHGMRLQITVDMDPVGRSVSEVTLRLLEAFQVEVKEHGEVCPANWK	185
QY	251	PGSETIIPDPAGKALK-YFDK	269
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	186	KGAPTMKPEPNASVEGYFSK	205

Search completed: January 17, 2003, 19:20:23
Job time : 18 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:17:48 : Search time 19 Seconds

(without alignments)
1371.180 Million cell updates/sec

Title: US-09-911-346-2

Perfect score: 1441

Sequence: 1 MEALPLLAATTPDHGRHRL.....GSEFTIPDPAGKLYPDKLN 271

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: pirl:*
2: pirl:*
3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1441	100.0	271	2	G01790
2	744	51.6	198	2	A57716
3	740	51.4	198	2	I68897
4	735.5	51.0	199	2	A46711
5	731.5	50.8	200	2	I51016
6	730.5	50.7	199	2	I52425
7	721.5	50.1	199	2	A48513
8	701	48.6	199	2	T16005
9	689	47.8	195	2	J00064
10	680	47.2	195	2	JC2258
11	639.5	44.4	226	2	S43598
12	634	44.0	192	2	T41413
13	588.5	40.8	203	2	A12385
14	588.5	40.8	210	2	T06318
15	584	40.5	196	2	A47362
16	582.5	40.4	265	2	T09211
17	570.5	39.6	200	2	S76284
18	568.5	39.5	242	2	S49173
19	567	39.3	196	2	S69732
20	548	38.0	199	2	S73193
21	479.5	33.3	233	2	S67947
22	477	33.1	178	2	S29119
23	477	33.1	200	2	A71689
24	474.5	32.9	199	2	F83540
25	474.5	32.9	273	2	A43862
26	467	32.4	202	2	C97756
27	461	32.0	200	2	G83204
28	455	31.6	195	2	G71492
29	451.5	31.3	200	2	AB0552

30	444	30.8	196	2	H85587	thio-specific anti
31	444	30.8	196	2	E72036	thio-specific anti
32	441.5	30.6	180	2	B69867	2-cys peroxiredoxi
33	440.5	30.6	200	2	AB0388	probable alkyl hyd
34	434.5	30.2	183	2	A83983	2-cys peroxiredoxi
35	434.5	30.2	207	2	E82287	antioxidant, Ahpc/
36	432.5	30.0	198	2	B81453	alkyl hydroperoxid
37	406.5	28.2	181	2	AD1275	2-cys peroxiredoxi
38	406.5	28.2	181	2	AD1538	2-cys peroxiredoxi
39	404	28.0	198	2	H71801	probable peroxidase
40	403	28.0	198	2	C64715	alkyl hydroperoxid
41	398.5	27.7	197	2	C84951	alkyl hydroperoxid
42	394.5	27.4	204	2	S78299	hypothetical prote
43	346.5	24.0	206	2	G82668	subunit C of alkyl
44	342	23.7	188	2	D71314	probable alkyl hyd
45	341	23.7	222	2	E70374	alkyl hydroperoxid

ALIGNMENTS

```
RESULT 1
G01790
probable thiol-specific reductase (EC 1.-.-.-) AOE37-2 - human
N:Alternate names: antioxidant enzyme AOE37-2
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 11-Jun-1999
C:Accession: G01790
R:jin, D.
submitted to the EMBL Data Library, April 1995
A:Reference number: G08418
A:Accession: G01790
A>Status: translated from GB/EMBL/DDB3
A:Molecule type: mRNA
A:Residues: 1-271 <JIN>
C:Superfamily: alkyl hydroperoxidase reductase c22 protein; alkyl hydroperoxidase c22 p
C:Keywords: oxidoreductase
F:88-229/Domain: alkyl hydroperoxidase c22 protein homology <C22>

Query Match      100.0%; Score 1441; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 1e-124;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEALPLLAATTPDHGRHRLDLLFLPAGAVOGMETEERRTRREECHFYAGGVY 60
Db 1 MEALPLLAATTPDHGRHRLDLLFLPAGAVOGMETEERRTRREECHFYAGGVY 60
OY 61 PGEASRVSADHSLSLSKAKISKAPYWEGRFAVIDGEFKELTDYNGKYLVEFFYPLDF 120
Db 61 PGEASRVSADHSLSLSKAKISKAPYWEGRFAVIDGEFKELTDYNGKYLVEFFYPLDF 120
OY 121 TFVCPTEIIAAGDRLEEFERSINTEVVACSVDSQETHLAWMPRROGGLGIRIPLSLDL 180
Db 121 TFVCPTEIIAAGDRLEEFERSINTEVVACSVDSQETHLAWMPRROGGLGIRIPLSLDL 180
OY 181 THQISKDYGVLVLEDSGHTLRGLFTIIDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDK 240
Db 181 THQISKDYGVLVLEDSGHTLRGLFTIIDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDK 240
OY 241 HGEVCPAGWKPGESEFTIIPDPAGKLYPDKLN 271
Db 241 HGEVCPAGWKPGESEFTIIPDPAGKLYPDKLN 271

RESULT 2
A57716
thiol-specific antioxidant - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 11-Jun-1999
C:Accession: A57716
R:Chae, H.-I.; Robison, K.; Poole, L.B.; Church, G.; Storz, G.; Rhee, S.G.
Proc. Natl. Acad. Sci. U.S.A. 91, 7017-7021, 1994
```


C:Accession: I51016
R:Rebsta, T.; Kamio, K.; Tajima, T.; Kaneda, T.; Suzuki, A.
Roux's Arch. Dev. Biol. 204, 400-405, 1995
A:Title: Pag gene-like protein (APB-25) of *Cynops* embryo: regional distribution and gene
A:Reference number: I51016
A:Accession: I51016
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-200 <TAB>
A:Cross-references: GR:DJ37808; NID:g520852; PIDN:BA07054.1; PID:g520853
A:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot
E:15-157/Domain: alkyl hydroperoxidase c22 protein homology <C22>

Query Match	50.8%	Score 731.5	DB 2	Length 200
Best Local Similarity	71.5%	Pred. No. 1.1e-59		
Matches 138	Conservative 22	Mismatches 32	Indels 1	Gaps 1

[illegible]

RESULT 6
 152425
 probable thioredoxin peroxidase (EC 1.11.1.-) HBP23 - rat
 N:Alternative names: heme-binding 23k protein (HBP23); proliferation associated protein P1
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 02-Jun-2000
 C:Accession: 152425

Query Match	50.7%;	Score 730.5;	DB 2;	Length 199;
Best Local Similarity	70.3%;	Pred. No. 1.4e-59;		
Matches 135; Conservative	24;	Mismatches 32;	Indels 1;	Gaps 1;

Qy	79	AktskPAPMEGTAVI-DGEKELKLTDYRGKYLVFEFFPLDFTPCPPETIIAFGRLEE	137
Db	6	AKIGHPASEKATVMPBGQFKDISLDYKGRKYVVEFFPLDFTFCPEIIIAFSRAEE	65
Qy	138	FRSINTFVMACSVDSOFHLMAMINTPRROGGGLPIRPLSLDTHOISMDGYVLEDSGH	197
Db	66	EKILNCOVIGASVSDFCHLMAINTPKQGGLGPMNIPVLVSDPKRTIAODYGLKADEGI	125
Qy	198	TLRGLFIIDDKGLIRQLITLANDLPVGRSVDETRLVQAFOYTKDHGEVCPAGMKGSETII	257
Db	126	SFRGLFIIDDKGLIRQLITNDLPVGRSVDIELRLVQAFOETDKHGECVPAGMGSGDTIK	185
Qy	258	PDPAGKLTIEDK 269	
Db	186	PDVNRSKKEYESK 197	

RESULT 7
A48513

Query Match	50.18;	Score 721.5;	DB 2;	Length 199;
Best Local Similarity	68.88;	Pred. No. 9.2e-59;		
Matches 132; Conservative	27;	Mismatches 32;	Indels 1;	Gaps 1;

[illegible]

RESULT 8
 T16005
 hypothetical protein F09E5.2 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T16005
 R:Chisoe, S.
 submitted to the EMBL Data Library, September 1995
 A:Description: The sequence of C. elegans cosmid F09E5.
 A:Reference number: Z18444
 A:Accession: T16005
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-576 <CHT>
 A:Cross-references: EMBL:U37429; NID:g1019949; PID:g1019951; PIDN:AAA79342.1; CESP:F09E5.2
 A:Experimental source: strain Bristol N2


```
RESULT 12
T41413
thioredoxin peroxidase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C/Accession: T41413; T50461
R/Mood: V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z21954
A:Accession: T41413
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-192 <MOO>
A:Cross-references: EMBL:AL031798; PIDN:CAA21182.1; GSPDB:GN00068; SPDB:SPCC576.03c
A:Experimental source: strain 972h(-); cosmid c576
R/Koo, K.H.; Kim, K.; Chae, H.Z.
submitted to the EMBL Data Library, August 1998
A:Description: Thioredoxin peroxidase from Schizosaccharomyces pombe.
A:Reference number: Z25073
A:Accession: T50461
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-192 <KOO>
A:Cross-references: EMBL:AF083335; PIDN:AAC71013.1
C:Genetics:
A:Gene: SPDB:SPCC576.03c
A:Map position: 3
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot

Query Match 44.0%; Score 634; DB 2; Length 192;
Best Local Similarity 60.0%; Pred. No. 9.6e-51;
Matches 114; Conservative 36; Mismatches 38; Indels 2; Gaps 1;

QY 80 KISPAWEGTAVIDSEFKELKLDYRGKYLVEFFPLDFTFVCPTETIAFGDRLEEF 139
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 QIGKPADDFGTAVVNGAFEEIKLADYKRWVFLGFYPLDFTFVCPTETIAFSAASKFA 63

QY 140 SINTEVAVCSVDQFTHLAMINPFRROGGGIPRIPLISDLTHQISKDYGLLEDSGHTL 199
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 ERNAQVILTSTSEYSHAIINPFRKGGGGINIPILAPSHKVSVDYGLLIDAGVAF 123

QY 200 RGLFIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDKHGVCAPGKRPGETIIP 259
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 RGLFLIDPKVLRQITLNDLPVGRSVDETLRLVQAFQVEBHGVCAPNMHKGSDTL--D 181

QY 260 PAGKLYFDR 269
||| |
Db 182 TKNPEKYSK 191

RESULT 13
A13385
peroxiredoxin [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C/Accession: A12385
R/Raneke, T.; Nakamura, Y.; Wolk, C.P.; Kurlitz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi,
N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; M0ID:2155285; PMID:11759640
A:Accession: A12385
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-203 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA076340.1; PID:q17133778; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr4641
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot
```

```
Query Match 40.8%; Score 588.5; DB 2; Length 203;
Best Local Similarity 57.1%; Pred. No. 1.6e-46;
Matches 108; Conservative 30; Mismatches 50; Indels 1; Gaps 1;

QY 80 KISPAWEGTAVIDSEFKELKLDYRGKYLVEFFPLDFTFVCPTETIAFGDRLEEF 139
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 12 RVGQAPDFATAVADQEFKIKSDYRGKVVLEFFPLDFTFVCPTETIAFSRDEEFK 71

QY 140 SINTEVAVCSVDQFTHLAMINPFRROGGGIPRIPLISDLTHQISKDYGLLEDSGHTL 199
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 72 KLNTIELGVSDSEFSLAWIOTDRKSGVGDNLVPLVSDIKKEVSDAVYNLDPAGIAL 131

QY 200 RGLFIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDKH-GEVCPAGKRPGETIIP 258
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 132 RGLFLIDPKVLRQITLNDLPVGRSVDETLRLVQAFQYTDKH-GEVCPAGKRPGETIIP 191

QY 259 DPAGKLYF 267
||| |
Db 192 DPVASKYVF 200

RESULT 14
T06318
thiol-specific antioxidant protein precursor homolog TSA - wheat (fragment)
C:Species: Triticum aestivum (common wheat)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 20-Jun-2000
C/Accession: T06318
R/Tsunoyama, Y.
submitted to the EMBL Data Library, January 1997
A:Reference number: Z15590
A:Accession: T06318
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-210 <TSD>
A:Cross-references: EMBL:AB000405; PIDN:BA119099.1
A:Experimental source: cv. Norin-no.61, seedlings
C:Genetics:
A:Gene: TSA
A:Genome: nuclear
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 p
C:Keywords: chloroplast
F:1-30/Domain: transit peptide (chloroplast) (fragment) #status predicted <TNP>
F:27-169/Domain: alkyl hydroperoxidase c22 protein homology <C22>
F:31-210/Product: thiol-specific antioxidant protein homology #status predicted <MAT>

Query Match 40.8%; Score 588.5; DB 2; Length 210;
Best Local Similarity 55.2%; Pred. No. 1.6e-46;
Matches 111; Conservative 33; Mismatches 52; Indels 5; Gaps 2;

QY 68 SVADSHLSKAKISKAPWEGTAVIDSEFKELKLDYRG-KYLVEFFPLDFTFVCPT 126
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 11 AAAYEDLPL---VGNKAPDFAAEAVDFQEFINKLSDYIGKRVILFFYPLDFTFVCPT 66

QY 127 EIIAFGRLEERSINTEVAVCSVDQFTHLAMINPFRROGGGIPRIPLISDLTHQISK 186
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 EIIAFGRLEERSINTEVAVCSVDQFTHLAMINPFRROGGGIPRIPLISDLTHQISK 126

QY 187 DYGVLLDSGHTLRLGFLIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCP 246
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 127 SFQVLIDPKVLRQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCP 186

QY 247 AGKRPGETIIPDPAGKLYF 267
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 187 AGKRPGETIIPDPAGKLYF 207

RESULT 15
A47362
thiol-specific antioxidant - yeast (Saccharomyces cerevisiae)
N/Alternate names: protein YML028W
C:Species: Saccharomyces cerevisiae
C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 11-Jun-1999
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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:15:03 ; Search time 39 Seconds

(without alignments)
925.921 Million cell updates/sec

Title: US-09-911-346-2

Perfect score: 1441

Sequence: 1 MEALPLAATPDHGHNRRL.....GSETIPDPAGLKYPDKIN 271

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470.

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
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12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1441	100.0	271	AAW12692	Natural killer cell
2	1441	100.0	271	AA143399	Human natural kill
3	1441	100.0	271	AAW50249	Human natural kill
4	1441	100.0	271	AAW82478	Natural killer cell
5	1441	100.0	271	AAW68038	Amino acid sequenc
6	854.5	59.3	242	AAW57947	Drosophila melanog
7	750.5	52.1	233	AA143528	Human cancer assoc
8	750.5	52.1	233	AAW41353	Human ovarian anti
9	746	51.8	198	AAW68036	Amino acid sequenc
10	721	50.0	198	AAW68040	Amino acid sequenc

11	719	49.9	198	AAU78580	Mouse peroxiredoxi
12	715	49.6	194	ABW58322	Drosophila melanog
13	715	49.6	194	ABW58323	Drosophila melanog
14	713.5	49.5	199	AAW09793	Natural killer cell
15	703	48.8	224	AAW56959	Human prostate can
16	703	48.8	256	AAW68037	Amino acid sequenc
17	691	48.0	219	ABW26215	Novel human diagno
18	682	47.3	199	AAW2715	Drosophila melanog
19	650	45.1	220	ABW61843	Drosophila melanog
20	637.5	44.2	181	AAW39938	NKEF sequence dedu
21	619	43.0	178	AAW09794	Natural killer cel
22	598	41.5	982	AAU71855	Leishmania antigen
23	598	41.5	1427	AAU71857	Leishmania MAP5A-
24	598	41.5	1641	AAU71856	Leishmania antigen
25	587	40.7	199	AAW70221	Leishmania antigen
26	587	40.7	199	ABW60873	Leishmania antigen
27	587	40.7	199	AAU71817	Leishmania antigen
28	586	40.7	206	AAW70222	Leishmania antigen
29	586	40.7	206	ABW60874	Leishmania antigen
30	586	40.7	206	AAU71818	Leishmania antigen
31	580	40.2	196	ABW62769	Drosophila melanog
32	571	39.6	271	AAW23833	Arabidopsis thalia
33	571	39.6	271	AAW45901	Arabidopsis thalia
34	571	39.6	273	AAW23832	Arabidopsis thalia
35	571	39.6	273	AAW45900	Arabidopsis thalia
36	567	38.9	196	AAW19092	Protein encoded by
37	561	38.9	194	AAW46775	Amino acid sequenc
38	557	38.7	266	AAW08191	Arabidopsis thalia
39	550.5	38.2	187	AAW62792	Tryparedoxin perox
40	513.5	35.6	147	AAW01615	Human secreted pro
41	507	35.2	224	ABW7458	Fungi stress respo
42	491	34.1	263	ABW3754	New flower bud ind
43	462	32.1	202	AAW13474	Protein encoded by
44	462	32.1	202	AAW83150	Protein encoded by
45	462	32.1	202	ABW94121	Chlamydia protein

ALIGNMENTS

RESULT 1	
AAW12692	
AAW12692 standard; Protein: 271 AA.	
XX	
AC	AAW12692:
XX	
DT	05-SEP-1997 (first entry)
XX	
DE	Natural killer cell enhancing factor C.
XX	
KW	Natural killer cell enhancing factor C; NKEF C; human; leukaemia cell;
KW	natural killer cell; lymphocyte; tumour cell; superoxide radical; LAK;
KW	lymphokine-activated killer cell; interleukin-2; growth inhibitor;
KW	enhanced cell proliferation; antioxidant; vesicular stomatitis virus;
KW	inhibitor; viral infection; inflammation; neoplasia; therapy.
XX	
OS	Homo sapiens.
XX	
PN	WO9639424-A1.
XX	
PD	12-DEC-1996.
XX	
PE	06-JUN-1995; 95WO-US07200.
XX	
PR	06-JUN-1995; 95WO-US07200.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Genetz R, Ni J, Rosen CA, Yu G;
XX	
DR	WPI: 1997-043059/04.
DR	N-FSDB; AAT51788.
XX	

PT DNA encoding human natural killer cell enhancing factor C - useful
 PT for preventing or treating viral infections, inflammation, neoplasia
 PT and damage from superoxide radicals

PS Claim 1; Fig 1; 61pp; English.

CC This sequence represents the human natural killer cell enhancing factor
 CC (NKEF) C. Natural killer cells (NK) are a subset of lymphocytes capable
 CC of lysing a variety of tumour cells without prior activation.
 CC Lymphokine-activated killer cells (LAK) are mainly NK cells activated by
 CC interleukin-2, and are capable of lysing wider ranges of tumour cells
 CC with higher cytotoxic activity. NK/LAK activity is influenced by various
 CC components of blood, including the NKEF A and B proteins. Transfection of
 CC NKEF into cells results in cell-type-dependent enhanced cell
 CC proliferation or growth inhibition. The NKEF proteins are antioxidants,
 CC but show no sequence homology to other antioxidants, such as catalase or
 CC superoxide dismutase. This sequence, or the DNA encoding it can be used
 CC to inhibit the cytopathic effect of vesicular stomatitis virus and to
 CC inhibit the growth of leukaemia cells, or to treat a patient in need of a
 CC NKEF C polypeptide. Disease or susceptibility to disease related to an
 CC under-expression of this protein can be diagnosed by determining a
 CC mutation in the DNA encoding this sequence. This protein can also be used
 CC to identify compounds which bind to and activate a receptor for it. The
 CC products can also be used to treat viral infections, inflammation,
 CC neoplasia and damage from superoxide radicals.

CC Sequence 271 AA:

Query Match 100.0%; Score 1441; DB 18; Length 271;
 Best Local Similarity 100.0%; Pred. No. 1,4e-147;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEALPLLAATTPDHGRHRLRLPLLLPLLPAGAVOGWETERRPRTRREECHFYAGGOVY 60
 DB 1 MEALPLLAATTPDHGRHRLRLPLLLPLLPAGAVOGWETERRPRTRREECHFYAGGOVY 60
 QY 61 PGEASRVSVADHSHLSKAKISKAPAWEGTAVIDGEFEKELTDYRGKYLVEFFYPDLF 120
 DB 61 PGEASRVSVADHSHLSKAKISKAPAWEGTAVIDGEFEKELTDYRGKYLVEFFYPDLF 120
 QY 121 TFVCPTEIIAFGDRLEEFRSINTEVAVCSVDSQFTHLAWINTPRROGGLGPIRIPLSLDL 180
 DB 121 TFVCPTEIIAFGDRLEEFRSINTEVAVCSVDSQFTHLAWINTPRROGGLGPIRIPLSLDL 180
 QY 181 THQISKDYGVYLEDSGHTLRGLFTIIDKGILROITLNDLPVGRSVDETLRLVQAFQYTDK 240
 DB 181 THQISKDYGVYLEDSGHTLRGLFTIIDKGILROITLNDLPVGRSVDETLRLVQAFQYTDK 240
 QY 241 HGEVCPAGWKPGSETIIPDPAGKLKTFDKLN 271
 DB 241 HGEVCPAGWKPGSETIIPDPAGKLKTFDKLN 271

RESULT 2

AA433399 standard; Protein; 271 AA.

AC AAY43399;
 XX
 DT 28-JUN-2000 (first entry)
 XX
 DE Human natural killer cell enhancing factor C protein sequence.
 XX
 KW Natural killer cell enhancing factor C; NKEF C; human; diagnosis; probe;
 KW viral infection; inflammation; neoplasia; superoxide radical damage;
 KW bone marrow rejection; therapy.
 XX
 OS Homo sapiens.
 XX
 PN US5985612-A.
 XX
 PD 16-NOV-1999.
 XX

PF 06-JUN-1995; 95US-0467265.
 XX
 PR 06-JUN-1995; 95US-0467265.
 XX

PA (YUGG/) YU G.
 PA (GENT/) GENTZ R.
 PA (ROSE/) ROSEN C A.
 PA (NIJ/) NI J.

PI Gentz R, Rosen CA, Yu G, Ni J;

DR WPI: 2000-012791/01.
 DR N-PDB: AA237242.

PT Isolated polynucleotides encoding human natural killer cell enhancing
 PT factor C, useful for preventing, diagnosing or treating viral
 PT infections, neoplasia and damage from superoxide radicals -
 PS Claim 1; Fig 1; 29pp; English.

CC This sequence is the human natural killer cell enhancing factor C
 CC (NKEF C) of the invention. NKEF C protein and DNA sequences can be used
 CC in the diagnosis, prevention and treatment of disorders associated with
 CC inappropriate expression and activity (normally reduced) of NKEF C and to
 CC augment the action of natural killer cells and proteins. The NKEF C
 CC sequences may be used to treat disorders such as viral infections,
 CC inflammation, neoplasia and damage from superoxide radicals. They may be
 CC administered to treat the above diseases by rectifying mutations or
 CC deletions in a patient's genome that affect the activity of NKEF C by
 CC expressing inactive proteins or to supplement the patients own production
 CC of NKEF C. Antisense nucleic acid molecules may be administered to down
 CC regulate NKEF C expression by binding with the cells own NKEF C genes and
 CC preventing their expression. The NKEF C DNA and antisense molecules may
 CC also be used as probes in diagnostic assays to detect and quantitate the
 CC presence of similar nucleic acid sequences in samples, and hence which
 CC patients may be in need of restorative therapy. They may also be used to
 CC study the expression and function of NKEF C and its role in metabolism.
 CC NKEF C fragments may be used as antigens in the production of antibodies
 CC against NKEF C and in assays to identify modulators (agonists and
 CC antagonists) of NKEF C expression and activity. Anti-NKEF C antibodies
 CC and NKEF C antagonists may also be used to down regulate NKEF C
 CC expression and activity. They may be used in this way to treat disorders
 CC such as the treatment of bone marrow rejection. The antibodies may also
 CC be used as diagnostic reagents for identifying the presence of NKEF C in
 CC samples.

CC Sequence 271 AA:

Query Match 100.0%; Score 1441; DB 21; Length 271;
 Best Local Similarity 100.0%; Pred. No. 1,4e-147;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEALPLLAATTPDHGRHRLRLPLLLPLLPAGAVOGWETERRPRTRREECHFYAGGOVY 60
 DB 1 MEALPLLAATTPDHGRHRLRLPLLLPLLPAGAVOGWETERRPRTRREECHFYAGGOVY 60
 QY 61 PGEASRVSVADHSHLSKAKISKAPAWEGTAVIDGEFEKELTDYRGKYLVEFFYPDLF 120
 DB 61 PGEASRVSVADHSHLSKAKISKAPAWEGTAVIDGEFEKELTDYRGKYLVEFFYPDLF 120
 QY 121 TFVCPTEIIAFGDRLEEFRSINTEVAVCSVDSQFTHLAWINTPRROGGLGPIRIPLSLDL 180
 DB 121 TFVCPTEIIAFGDRLEEFRSINTEVAVCSVDSQFTHLAWINTPRROGGLGPIRIPLSLDL 180
 QY 181 THQISKDYGVYLEDSGHTLRGLFTIIDKGILROITLNDLPVGRSVDETLRLVQAFQYTDK 240
 DB 181 THQISKDYGVYLEDSGHTLRGLFTIIDKGILROITLNDLPVGRSVDETLRLVQAFQYTDK 240
 QY 241 HGEVCPAGWKPGSETIIPDPAGKLKTFDKLN 271
 DB 241 HGEVCPAGWKPGSETIIPDPAGKLKTFDKLN 271

```
RESULT 3
AAM50249
ID AAM50249 standard; Protein; 271 AA.
XX
AC AAM50249;
XX
DT 21-JAN-2002 (first entry)
XX
DE Human natural killer cell enhancing factor C.
XX
KM Natural killer cell enhancing factor C; NKEF C; human; antiviral,
KW virucide; antiinflammatory; cytostatic; antioxidant; vulnerary;
XX therapy; diagnosis.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT /label= Signal_peptide
FT 31..271
FT Protein /label= Mature_protein
FT
XX
PN US6294164-B1.
XX
PD 25-SEP-2001.
XX
PF 29-SEP-1999; 99US-0407891.
XX
PR 06-JUN-1995; 95US-0467265.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI NI J, Yu G, Gentz R, Rosen CA;
XX
DR WPI: 2001-647258/74.
DR N-PSDB: AAI70524.
XX
PT Natural killer cell enhancing factor C polypeptides encoded by the cDNA
PT in ATCC Deposit No. 97157, useful for preventing or treating viral
PT infections, inflammation, neoplasia or damage from superoxide radicals,
PT e.g. tissue injury -
XX
PS Claim 1; Fig 1; 29pp; English.
XX
CC The present sequence is that of human natural killer cell enhancing
CC factor C (NKEF C), as deduced from a cDNA clone (see AAI70524)
CC isolated from a cDNA library derived from cyclohexamide-treated
CC CEM cells. NKEF C is structurally related to highly conserved
CC oxidative stress proteins and shows 68% identity and 83% similarity
CC to NKEF B. NKEF C is highly expressed in heart, liver, skeletal
CC muscle, pancreas, testis and ovary, moderately expressed in
CC placenta, lung, prostate, small intestine and colon, and lowly
CC expressed in brain, spleen, thymus and peripheral blood leucocytes.
CC NKEF C polypeptide is useful for preventing and/or treating viral
CC infections, inflammation, neoplasia or damage from superoxide
CC radicals (e.g. tissue injury or ageing). The polypeptide may also
CC be used for inhibiting the cytopathic effect of vesicular stomatitis
CC virus and for inhibiting the growth of leukaemia cells. The
CC polypeptide and polynucleotide are also useful as research reagents,
CC for constructing DNA vectors, and for developing therapeutics and
CC diagnostics for treating human disease. Polypeptide fragments of
CC NKEF C that have growth inhibitory or antiviral activity are
CC claimed.
XX
SQ Sequence 271 AA;
XX
Query Match 100.0%; Score 1441; DB 22; Length 271;
Best Local Similarity 100.0%; Pred No. 1.4e-147;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEALPLLAATTPDHGRHRLLLPLLLFLPAGAVOGWETEEPRRTREEDCHFVAGGQVY 60
DB 1 MEALPLLAATTPDHGRHRLLLPLLLFLPAGAVOGWETEEPRRTREEDCHFVAGGQVY 60
```

```
QY 61 PGEASRVSVADHSLHLSKAKISKAPYWEQTAVIDEFEKLTLDYRGKLVFFFPYLPD 120
DB 61 PGEASRVSVADHSLHLSKAKISKAPYWEQTAVIDEFEKLTLDYRGKLVFFFPYLPD 120
QY 121 TFCVPTETIIAFGDRLEEFPSINTEVVACSVDSQFTHLAMINPRROGGLGPIRILPLSD 180
DB 121 TFCVPTETIIAFGDRLEEFPSINTEVVACSVDSQFTHLAMINPRROGGLGPIRILPLSD 180
QY 181 THOISKDYGYLDESGHTLGLFIIDDKGILRQITLNDLPVGSVDETLLVQAFQYTDK 240
DB 181 THOISKDYGYLDESGHTLGLFIIDDKGILRQITLNDLPVGSVDETLLVQAFQYTDK 240
QY 241 HGEVCPAGMKPGSETIIPDPAGKLYEDKLN 271
DB 241 HGEVCPAGMKPGSETIIPDPAGKLYEDKLN 271
RESULT 4
AAB82478
ID AAB82478 standard; Protein; 271 AA.
XX
AC AAB82478;
XX
DT 22-AUG-2001 (first entry)
XX
DE Natural killer cell enhancing factor C.
XX
KM Natural killer cell enhancing factor C; NKEF C; human; antioxidant;
KW vulnerary; antiinflammatory; virucide; antitumour; therapy;
XX diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT /label= Signal_peptide
FT 31..271
FT Protein /label= Mature_protein
FT
XX
PN US625079-B1.
XX
PD 03-JUL-2001.
XX
PF 06-JUN-1995; 95US-0467265.
XX
PR 06-JUN-1995; 95US-0467265.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI NI J, Yu G, Gentz R, Rosen CA;
XX
DR WPI: 2001-396982/42.
DR N-PSDB: AAF90573.
XX
PT Isolated polynucleotides encoding human natural killer cell enhancing
PT factor C, useful for preventing, diagnosing or treating viral
PT infections, neoplasia and damage from superoxide radicals -
XX
PS Claim 1; Fig 1; 49pp; English.
XX
CC The present sequence is that of human natural killer cell enhancing
CC factor C (NKEF C). NKEF C is highly expressed in heart, liver,
CC skeletal muscle, pancreas, testis and ovary, moderately in
CC placenta, lung, prostate, small intestine and colon, and lowly
CC expressed in brain, spleen, thymus and peripheral blood
CC leucocytes. cDNA (see AAF90573) encoding NKEF C was derived from
CC cyclohexamide-treated CEM cells. The protein shows 83.3% amino
CC acid similarity to NKEF B, and shows significant homology to several
CC other proteins. The invention provides NKEF C polypeptides, especially
CC a polypeptide comprising amino acids 1-271, 2-271 or 31-271 of the
CC present sequence, isolated nucleic acids encoding them, and methods
```

CC of producing the polypeptides in recombinant host cells. The NKEF
 CC C polypeptides and polynucleotides can be used to inhibit the
 CC growth of leukemia cells, to treat viral infection, to augment the
 CC effects of NK protein, to treat neoplasias such as tumours and
 CC cancers, to prevent inflammation, and to prevent damage from
 CC superoxide radicals in the body e.g. in tissue injury and ageing.
 CC The polypeptides can also be used to screen for potential agonists
 CC and antagonists of NKEF C activity. Antagonists may be useful in
 CC the treatment of bone marrow transplant rejection.

SO Sequence 271 AA:

Query Match 100.0%; Score 1441; DB 22; Length 271;
 Best Local Similarity 100.0%; Pred. No. 1.4e-147;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEALPLAATTPDHGRHRLRLPLFLPLPAGAVQGWETEERPRTRREECHFYAGGVY 60
 DB 1 MEALPLAATTPDHGRHRLRLPLFLPLPAGAVQGWETEERPRTRREECHFYAGGVY 60
 QY 61 PGEASRVSVADHSIHLAKISKAPAPYEGTAVIDGEFKEKLTIDYRGKYLVEFFYPLDF 120
 DB 61 PGEASRVSVADHSIHLAKISKAPAPYEGTAVIDGEFKEKLTIDYRGKYLVEFFYPLDF 120
 QY 121 TFVCPTEIIAFGDRLEEFRSINTEVACSVDSQFTHLAMINTPRROGGLPIRIPLSDL 180
 DB 121 TFVCPTEIIAFGDRLEEFRSINTEVACSVDSQFTHLAMINTPRROGGLPIRIPLSDL 180
 QY 181 THOISKDYGVLDSGHTLRGLFIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDK 240
 DB 181 THOISKDYGVLDSGHTLRGLFIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDK 240
 QY 241 HGEVCPAGMKPGSETIIPDPAGKLYFDKLN 271
 DB 241 HGEVCPAGMKPGSETIIPDPAGKLYFDKLN 271

RESULT 5

ABB68038
 ID AAB68038 standard; peptide: 271 AA.

AC AAB68038;

DT 29-JUN-2001 (first entry)

DE Amino acid sequence of the acid form of peroxylredoxin TXN.

KW Peroxylredoxin; acid form; oxidative stress; cell death; cancer;
 KW autoimmune disease; neurodegeneration; metabolic disorder.

OS Homo sapiens.

PN FR2798672-A1.

PD 23-MAR-2001.

PF 17-SEP-1999; 99FR-0011663.

PR 17-SEP-1999; 99FR-0011663.

PA (COMS) COMMISSARIAT ENERGIE ATOMIQUE.

PI Rab11loud T;

DR WPI: 2001-259869/27.

Purified acid form of peroxylredoxin, a marker of oxidative stress,
 PT useful in diagnosis and for identifying potential apoptotic and
 PT anti-apoptotic agents comprises a specific amino acid motif close to
 the active site -
 XX
 XX
 PS Claim 12; Page 23-24; 28pp; French.

CC The present sequence represents the acid form of a human peroxylredoxin
 CC enzyme. The acid form of peroxylredoxin is a characteristic marker of
 CC oxidative stress that can be measured simply and quickly, providing a
 CC reliable indication of stress even where this is of short duration.
 CC Modulators of the acid form of peroxylredoxin enzyme are used for the
 CC stimulation or inhibition of apoptosis. Compounds that stimulate
 CC formation of the acid form of peroxylredoxin are used to induce cell
 CC death (treatment of cancer and autoimmune diseases) while those that
 CC inhibit its formation are used to prevent cell death (treatment of
 CC neurodegeneration). Measuring the ratio between acid form and the native
 CC form of peroxylredoxin is used to diagnose metabolic disorders associated
 CC with oxidative stress.

SO Sequence 271 AA:

Query Match 100.0%; Score 1441; DB 22; Length 271;
 Best Local Similarity 100.0%; Pred. No. 1.4e-147;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEALPLAATTPDHGRHRLRLPLFLPLPAGAVQGWETEERPRTRREECHFYAGGVY 60
 DB 1 MEALPLAATTPDHGRHRLRLPLFLPLPAGAVQGWETEERPRTRREECHFYAGGVY 60
 QY 61 PGEASRVSVADHSIHLAKISKAPAPYEGTAVIDGEFKEKLTIDYRGKYLVEFFYPLDF 120
 DB 61 PGEASRVSVADHSIHLAKISKAPAPYEGTAVIDGEFKEKLTIDYRGKYLVEFFYPLDF 120
 QY 121 TFVCPTEIIAFGDRLEEFRSINTEVACSVDSQFTHLAMINTPRROGGLPIRIPLSDL 180
 DB 121 TFVCPTEIIAFGDRLEEFRSINTEVACSVDSQFTHLAMINTPRROGGLPIRIPLSDL 180
 QY 181 THOISKDYGVLDSGHTLRGLFIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDK 240
 DB 181 THOISKDYGVLDSGHTLRGLFIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDK 240
 QY 241 HGEVCPAGMKPGSETIIPDPAGKLYFDKLN 271
 DB 241 HGEVCPAGMKPGSETIIPDPAGKLYFDKLN 271

RESULT 6

ABB57947
 ID ABB57947 standard; Protein: 242 AA.

AC ABB57947;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 633.

KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

OS Drosophila melanogaster.

PN MO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.

PA (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI: 2001-656860/75.

DR N-PSDB; ABL02050.

New isolated nucleic acid detection reagent for detecting 1000 or more
 genes from Drosophila and for elucidating cell signalling and cell-cell

[illegible]

Query Match	Best Local Similarity	Score	DB	Length
Matches 139; Conservative	52.1%;	750.5;	DB 21;	233;
	67.1%;	Pred. No. 8e-73;		
	27;	Mismatches 40;	Indels 1;	Gaps 1;
QY 64	ASRSVADSHLSLAKRAISKRPAPVEGTAIVT-DGEFKELKLDYRGKXYLVFFPYLDFTF	122		
DB 25	ATCVCTADRKMSNGKSIKIGHFAPNFKATPVPDGGFDKSIDYKGYVFFPYLDFTF	84		
QY 123	VEPTFLIAFGDLDEFRSINTEVAVACSVDSTHIAWINTPRGGGLGRIIRPLSDLTN	182		
DB 85	VEPTFLIAFGDLDEFRSINTEVAVACSVDSTHIAWINTPRGGGLGRIIRPLSDLTN	144		
QY 183	QISKRYGLVEBSGHTLRGLFTIIDKGLIRQTLTNDLPGRSVDETLRLVQAFOYTDKNG	242		
DB 145	TLAAGDYGLAKADEGISFRGLFTIIDKGLIRQTLTNDLPGRSVDETLRLVQAFOYTDKNG	204		
QY 243	EVCAPGAKRGSEFTIIPDPAGKLKLYFDK	269		
DB 205	EVCAPGAKRGSEFTIIPDPAGKLKLYFDK	231		
RESULT 8	ABPA1353			
ID	ABPA1353 standard; Protein; 233 AA.			
XX AC	ABPA1353;			
XX DT	23-AUG-2002 (first entry)			
XX DE	Human ovarian antigen HCOO501, SEQ ID NO:2485.			
KW	Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;			
KW	ovarian cancer; breast cancer; reproductive system disorder;			
KW	infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;			
KW	PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;			
KW	inflammatory condition; immune disorder; blood disorder;			

The invention relates to 2175 novel human ovarian antigens (ABP411054-ABP43328) and to cDNAs encoding them (ABO54131-ABO56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognostic or preventing various ovarian and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune disorders (e.g., systemic lupus erythematosus) and blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders, and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WFO at ftp://ftp.wipo.int/pub/published_pct/sequences.

Query Match	52.1%	Score 750.5	DB 23	Length 233
Best Local Similarity	67.1%	Pred. No. 8e-73		
Matches 139	Conservative 27	Mismatches 40	Indels 1	Gaps 1

[illegible]

RESULT 9	
AAB68036	
ID	AAB68036 standard; peptide; 198 AA.
XX	
AC	AAB68036;
XX	
DT	29-JUN-2001 (first entry)

XX
KM
NW
AM
XX

05 Homo sapiens.

PN FR2798672-A1.

PD 23-MAR-2001.

17-SEP-1999: 99FB-0011663

AA 17-SEP-1999: 99FB-0011663
PR

PA (COMS) COMMISSARIAT ENERGIE ATOMIQUE.

PI Rabl1loud T;

DR WPI; 2001-259869/27.

PT Purified acid form of peroxylredoxin, a marker of oxidative stress,
PT useful in diagnosis and for identifying potential apoptotic and
PT anti-apoptotic agents and for identifying potential apoptotic and
PT the active site -
PT

PS Claim 12; Page 21-22; 28pp; French.

The present sequence represents the acid form of a human peroxiredoxin enzyme. The acid form of peroxiredoxin is a characteristic marker of oxidative stress that can be measured simply and quickly, providing a reliable indication of stress even where this is of short duration. Modulators of the acid form of peroxiredoxin enzyme are used for the stimulation or inhibition of apoptosis. Compounds that stimulate formation of the acid form of peroxiredoxins are used to stimulate death (treatment of cancer and autoimmune diseases) while those that inhibit its formation are used to prevent cell death (treatment of neurodegeneration). Measuring the ratio between acid form and the native form of peroxiredoxin is used to diagnose metabolic disorders associated with oxidative stress.

Query Match	51.88;	Score 746;	DB 22;	Length 198;
Best Local Similarity	70.58;	Pred. No. 2e-72;		
Matches 136;	Conservative 26;	Mismatches 31;	Indels 0;	Gaps 0

[illegible]

Db 93 VNCVVAVSVDSHFSHLAMINTPRKNGGIGHMNTIALLSDLTKOISRXYGVLEGGSLAR 152
Qy 201 GLFIIDDKGILROITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGWPGSEITIIPDP 260
Db 153 GLFIIDPNCVIRKHLNVNDLPVGRSVETLRLVKAFOYVETHGEVCPANWTPDSPTIKPS 212
Qy 261 AGKLYEDKLN 271
Db 213 AASKEYFOKVN 223

Search completed: January 17, 2003, 19:18:23
Job time : 41 secs

Result	Query	Description			
No.	Score	Match	length	DB	ID
1	1296	89.9	274	6	Q9BG12
2	1286.5	87.9	273	11	Q9Z0V5
3	877	60.9	223	5	Q9BI6F
4	854.5	59.3	242	5	Q9V3Q4
5	749	52.0	199	6	Q9BG13
6	734	50.9	199	5	Q9Y082
7	733	50.9	198	11	Q9CWM4
8	727	50.5	198	11	Q88376
9	723.5	50.2	199	11	Q9UKY1
10	721.5	50.1	199	9	Q9BG14
11	721.5	50.1	199	13	Q93241
12	721	50.0	195	5	Q9NM98
13	718.5	49.9	199	11	Q9CWM2
14	718	49.8	198	11	Q9DB49
15	717	49.8	196	5	Q8MSF6
16	715	49.6	194	5	Q9V3P0

17	708	49.1	193	5	08W002	08W02 osterlagia
18	702.5	48.8	199	3	09I886	09I886 oncorhynchu
19	701	48.6	576	15	019285	019285 caenorhabdl
20	695	48.2	199	5	076452	076452 onchocerca
21	695	48.2	247	5	08T416	08T416 acanthocheil
22	688	47.7	199	5	044941	044941 onchocerca
23	683	47.4	199	5	016026	016026 difflorilaria
24	679	47.1	199	5	044366	044366 onchocerca
25	678	47.1	193	5	09GUB2	09GUB2 litomosoid
26	676	46.9	199	5	016006	016006 difflorilaria
27	676	46.9	257	11	09Z0V6	09Z0V6 rattus norvi
28	673.5	46.7	219	5	09GN76	09GN76 schistosoma
29	654.5	45.4	193	5	08T6C4	08T6C4 echinococcu
30	650	45.1	220	5	09PE03	09PE03 dirosophila
31	650	45.1	234	5	09GP03	09GP03 dirosophila
32	647.5	44.9	185	5	096380	096380 echinococcu
33	642	44.6	226	5	09GU47	09GU47 trypanosoma
34	640	44.4	226	5	079469	079469 trypanosoma
35	634	44.0	192	3	074887	074887 schizosacch
36	629	43.7	185	5	097161	097161 schistosoma
37	617.5	42.9	226	5	095089	095089 schistosoma
38	613.5	42.6	226	5	09U185	09U185 leishmania
39	614.5	42.6	235	10	09FE86	09FE86 chlamydomon
40	609.5	42.3	199	5	086753	086753 trypanosoma
41	605	42.0	199	10	09FNS2	09FNS2 chlamydomon
42	595.5	41.3	199	5	08WSH1	08WSH1 trypanosoma
43	594	41.2	194	5	09Y0D3	09Y0D3 schistosoma
44	591	41.0	199	5	09T2S4	09T2S4 leishmania
45	588.5	40.8	203	16	08VNC5	08VNC5 anabaena sp

ALIGNMENTS

RESULT 1			
Q9BG12			
ID	Q9BG12	PRELIMINARY;	PRT; 274 AA.
AC	Q9BG12;		
DT	01-JUN-2001 (TrEMBLrel. 17, Created)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE	Peroxiredoxin 4.		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovidae; Bovine; Bos.		
OX	NCBI_taxid=9913;		
RN	[1]		
SEQUENCE FROM N.A.			
RP	TISSUE=LIVER;		
RC	Levens G., Donnay I., Knoops B.;		
RA	"Cloning of 4 new bovine peroxiredoxins, and screening of the complete		
RT	peroxiredoxin family in different bovine tissues."		
RL	Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.		
DR	EMBL; AF305563; AAC53660.1; -		
DR	HSSP; P30041; IPRX_33561		
DR	InterPro; IPR000866; Ahpc-TSA.		
DR	Pfam; PF00578; Ahpc-TSA; 1.		
QO	SEQUENCE 274 AA: 30741 NM; AEI4176CFIC70E37 CRC64;		

Query Match	89.98;	Score 1296;	DB 6;	Length 274;
Best Local Similarity	92.18;	Pred. No. 2.7e-116;		
Matches 246;	Conservative 8;	Mismatches 13;	Indels 0;	Gaps 0;

Qy	5	PLAAATPDHNRHLLPLPLLELLPAGVANGQETERTRETRREBECHFPAGAGGVGEA	64
	1	1 1	
Db	8	PLPLATTLAAGRSKLLPLPLLELLAAVAVGAEAEERPRTRREBECHFPAGAGGVGEV	67
Qy	65	SRVAVADHSLHSLAKISKRPARYWEGNAVVDGERKELKLDYRGKYLVEFFPYPLDPTFVC	124
	1	1 1	
Db	68	SRVAVAEHSLSLAKISKRPARYWEGNAVVDGERKELKLDYRGKYLVEFFPYPLDPTFVC	127
Qy	125	PTETIAAGCDRLREERSINTEVAVASVQSFTHLAWINTPRQGGAGIRIRPLSLDLTHQI	184

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Db 128 PRELIATFAGRIIDEFRSINTEVACVSDFTHLAWINTPRROGGLSINIMPLILDLNHQI 187
OY 185 SKDGYVLEDSGHTLRGLFIIDDKGILRQITLNDLPVGRSVETLRYNAFOYTDKHGEV 244
Db 188 SKDGYVLEDSGHTLRGLFIIDDKGILRQITLNDLPVGRSVETLRYNAFOYTDKHGEV 247
OY 245 CPAGMKPGSETIIPDPACKLKYFDKLN 271
Db 248 CPAGMKPGSETIIPDPACKLKYFDKLN 274

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RESULT 2

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O920V5 PRELIMINARY: PRT: 273 AA.
ID O920V5
AC O920V5;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PRX IV.
CN PRX IV.
OC Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99148808; Pubmed=10025941;
RA Matsunoto A., Okado A., Fujii T., Fujii J., Egashira M., Mikawa N.,
RA Taniguchi N.;
RT "Cloning of the peroxiredoxin gene family in rats and characterization
RT of the fourth member.";
RL FEBS Lett. 443:246-250(1999).
DR EMBL; AF106945; AAD17993.1;
DR HSSP; P30041; 1PRX.
DR InterPro; IPR000866; Ahpc-TSA.
DR Pfam; PF00578; Ahpc-TSA; 1.
SQ SEQUENCE 273 AA; 31007 MW; 09E614794F1DC6C2 CRC64;

```

Query Match 87.9%; Score 1266.5; DB 11; Length 273;
 Best Local Similarity 90.3%; Pred. No. 1.8e-113;
 Matches 242; Conservative 10; Mismatches 13; Indels 3; Gaps 2;

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OY 6 LLAATTPDHGRHRLLL--PLLEFLPAGAVOGMETEERPRTRRECHFAVGQVPE 63
Db 7 LLDGTPPSR-RMRKLVLLPLPLFLQLQTEALGLESDDFRFRRENCHRYAGQVPE 65
OY 64 ASRVSVADHSLHLSKATISKRPARYWESTAVIDGFEKELTDYRGKYLVEFFYPLDFTFV 123
Db 66 VSRVSVADHSLHLSKATISKRPARYWESTAVINGEFKELTDYRGKYLVEFFYPLDFTFV 125
OY 124 CPTEIIAFGDRLEEFPSINTEVACVSDFTHLAWINTPRROGGLSINIMPLILDLTHQ 183
Db 126 CPTEIIAFGDRLEEFPSINTEVACVSDFTHLAWINTPRROGGLSINIMPLILDLTHQ 185
OY 184 ISKDYGVLEDSGHTLRGLFIIDDKGILRQITLNDLPVGRSVETLRYNAFOYTDKHGE 243
Db 186 ISKDYGVLEDSGHTLRGLFIIDDKGILRQITLNDLPVGRSVETLRYNAFOYTDKHGE 245
OY 244 VCPAGMKPGSETIIPDPACKLKYFDKLN 271
Db 246 VCPAGMKPGSETIIPDPACKLKYFDKLN 273

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RESULT 3

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O9BIF6 PRELIMINARY: PRT: 223 AA.
ID O9BIF6
AC O9BIF6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Thioresdoxin peroxidase Bgtrp (fragment).
OS Biomphalaria glabrata (Bloodfluke planorb).

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OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Planorbidae; Biomphalaria.
OX NCBI_TaxID=6526;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=LAC; TISSUE=ALBUMEN GLAND;
RA Cousin C., Ofori K., Okulate M., Grant J., Richards C., Lewis F.,
RA Knight M.;
RT "Biomphalaria glabrata: Molecular differences between the albumen
RT glands of susceptible and non-susceptible snails.";
RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY026258; AAK26236.1;
DR HSSP; P30041; 1PRX.
DR InterPro; IPR000866; Ahpc-TSA.
DR Pfam; PF00578; Ahpc-TSA; 1.
DR Non-Ter
FT NON-TER
SQ SEQUENCE 223 AA; 25033 MW; B5B995442C1B906 CRC64;

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Query Match 60.9%; Score 877; DB 5; Length 223;
 Best Local Similarity 76.5%; Pred. No. 3.7e-76;
 Matches 163; Conservative 18; Mismatches 30; Indels 2; Gaps 1;

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OY 55 AGGOVYVGEASRVSVADHSLHLSKATISKRPARYWESTAVIDGFEKELTDYRGKYLVEF 114
Db 5 AGGOVYVGEASRVSVADHSLHLSKATISKRPARYWESTAVIDGFEKELTDYRGKYLVEF 62
OY 115 FYPLDFFVCPTEIIAFGDRLEEFPSINTEVACVSDFTHLAWINTPRROGGLSINIM 174
Db 63 FYPLDFFVCPTEIIAFGDRLEEFPSINTEVACVSDFTHLAWINTPRROGGLSINIM 122
OY 175 PLSLDLTHQISKDYGVLEDSGHTLRGLFIIDDKGILRQITLNDLPVGRSVETLRYNA 234
Db 123 PLSLDLTHQISKDYGVLEDSGHTLRGLFIIDDKGILRQITLNDLPVGRSVETLRYNA 182
OY 235 FOYTDKHGEVCPAGMKPGSETIIPDPACKLKYF 267
Db 183 FOYTDKHGEVCPAGMKPGSETIIPDPACKLKYF 215

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RESULT 4

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O9V304 PRELIMINARY: PRT: 242 AA.
ID O9V304
AC O9V304;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CG1274 protein (SECRETABLE thioresdoxin peroxidase) (GH2379P).
GN JAFRAC2 OR CG1274.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196006; Pubmed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutcon G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Piankoff C., Balowin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu U., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borzova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertler S., Fleischmann W.,

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RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ideguchi C.,
RA Jaleil M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusserkern D.R., Paclob J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein J., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhan G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RL "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-20098524; PubMed-10632718;
RA Rodriguez J., Agudo M., Van Damme J., Vandekerckhove J.,
RA Santaren J.F.,
RT "Polypeptides differentially expressed in imaginal discs define the
RT peroxiredoxin family of genes in *Drosophila*."
RL Eur. J. Biochem. 267:487-497(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Raayak S.N., Spinola B., Klichko V.I., Orr W.C.,
RT "Cloning, expression and characterization of the peroxiredoxin gene
RT family in *Drosophila melanogaster*."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuncio J., Paclob J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celinker S.,
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AEO03476; AAF47704.1; -
DR EMBL: AF167099; AAF42986.1; -
DR EMBL: AF321614; AAK06769.1; -
DR EMBL: AY060785; AAL28333.1; -
DR FLYBase; FBgn0040308; Jafnac2.
DR InterPro: IPR000866; Ahpc-TSA.
DR Pfam: PF00578; Ahpc-TSA; 1.
KW Peroxidase.
SQ SEQUENCE 242 AA; 26743 MW; 8A0142FB19D9564 CRC64;

Query Match 59.3%; Score 854.5; DB 5; Length 242;
Best Local Similarity 65.2%; Pred. No. 6.1e-74;
Matches 161; Conservative 29; Mismatches 48; Indels 9; Gaps 2;

QY 25 LLLFLPAGAVOGWETTERPRTRREECHHFYAGGVYGPGEASVYADSLHLSKAKISKP 84
DB 5 LSVLLLSAALVGAKPED-----NESCISFAGSGVYPPDQPK-----GDHQLQYTKAVISKP 55
QY 85 APYMEGTAVIDGEFKELKLTDRGKYLVFFYPLDFTFVCPTEIITAFSDRLSEFSRINT 144
DB 56 APQEGTAIVNKEIYKLSQYLGKYVLLFPLDFTFVCPTEIITAFSDRIAEFKIKTE 115
QY 145 VVACSVDSQFTHLAININPRROGGIGPRTIRPLSLDTHQISDXYLYEDSHTIRGLFI 204
DB 116 VIGVSVDSHFTHLAININPRKREGGIGDVKIPLLSLDTHKISDXYLYESSGHALRGFI 175
QY 205 IDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGKPKPSETIIPPACKL 264

DB 176 IDQTCVLRQITMNDLPVGRSVDETLRLVQAFQYTDTHGEVCPAGKPKPADITIVPPEKXT 235
QY 265 KYFDKLN 271
DB 236 KYFAKNM 242

RESULT 5
QYBG13 PRELIMINARY; PRT; 199 AA.
AC QYBG13;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE Bos taurus (bovine).
OS Bos taurus (bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RA Leyens G., Donnay I., Knops B.,
RT "Cloning of 4 new bovine peroxiredoxins, and screening of the complete
RT peroxiredoxin family in different bovine tissues."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF305562; AAC53659.1; -
DR HSSP: P30041; IPRX.
DR InterPro: IPR000866; Ahpc-TSA.
DR Pfam: PF00578; Ahpc-TSA; 1.
SQ SEQUENCE 199 AA; 21946 MW; 5F256CE54090E2DE CRC64;

Query Match 52.0%; Score 749; DB 6; Length 199;
Best Local Similarity 69.1%; Pred. No. 6.4e-64;
Matches 134; Conservative 26; Mismatches 34; Indels 0; Gaps 0;

QY 78 KAKISKPAPEYMEGTAVIDGEFKELKLTDRGKYLVFFYPLDFTFVCPTEIITAFSDRLSE 137
DB 6 KAHVGKPAPEFQATVAVVGAFREKVLSDYKGYVLLFPLDFTFVCPTEIITAFSDRAAE 65
QY 138 FRSINTEVACSVDSQFTHLAININPRROGGIGPRTIRPLSLDTHQISDXYLYEDSGH 197
DB 66 FHLKCEVGVASVDSQFTHLAININPRKREGGIGPRTIRPLSLDTHQISDXYLYEDSGH 125
QY 198 TLRLGLFIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGKPKPSETI 257
DB 126 AYRGFLVIDKGVLRQVITINDLPVGRSVDEALRLVQAFQYTDHGEVCPAGKPKPSDTIK 185
QY 258 PDPAGKLYFDKLN 271
DB 186 PNVDSKKEYFSKHN 199

RESULT 6
QY082 PRELIMINARY; PRT; 199 AA.
AC QY082;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, last annotation update)
DE Peroxiredoxin.
GN TPX-1.
OS Glabodera rostochiensis (Golden nematode).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
OC Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
OX NCBI_TaxID=31243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ROL;
RX MEDLINE-20542028; PubMed-11087915;
RA Robertson L., Robertson W.M., Sobczak M., Helder J., Tetaud E.,

RA Arlyanayagam M.R., Ferguson M.A.J., Fairlamb A., Jones J.T.;
 RT "Cloning, expression and functional characterization of a
 RL peroxiredoxin from the potato cyst nematode *Globodera rostochiensis*.";
 DR EMBL: AJ243736; CAB48391.1; -.
 DR HSSP: P30041; 1PRX.
 DR InterPro: IPR000866; Ahpc-TSA.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 SO SEQUENCE 199 AA; 22317 MW; 90AD8274672B0F53 CRC64;

Query Match 50.9%; Score 734; DB 5; Length 199;
 Best Local Similarity 67.4%; Pred. No. 1.8e-62;
 Matches 130; Conservative 30; Mismatches 33; Indels 0; Gaps 0;

QY 77 SAATGKPPAPYEGTAVIDGFEKELKLDYRGKYLVFFFPYPLDFTFVCPTETIAFGDRLE 136
 DB 5 SAATGKPPAPYEGTAVIDGFEKELKLDYRGKYLVFFFPYPLDFTFVCPTETIAFGDRLE 136
 QY 137 EFRSINTEVAVCSVDSQFTHLAWINTPRROGGLGPIRIPILSDLTHTQISKDYGVLEDSG 196
 DB 65 EFKKIDTQIACSTDSKSFHLEINKPRHGGGLGEMKIPVLADTNHKKISRDYGVLMEEHG 124
 QY 197 HTLRLFTIIDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETI 256
 DB 125 IAFRLFTIIDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETI 184
 QY 257 IPPDAGKLYFPDK 269
 DB 185 KPDEGSGQFFPK 197

RESULT 7

QY 09CWM4 PRELIMINARY; PRT; 198 AA.
 AC 09CWM4;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Peroxiredoxin 2.
 GN PRDX2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RX STRAIN=C57BL/6J; TISSUE=EMBRYONIC STEM CELLS;
 RA MEDLINE=21085660; PubMed=11217851;
 RA Kawai T., Shinaagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Schirml L.M., Staudl F., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staudl F., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK010653; BAB27093.1; -.
 DR HSSP: P30041; 1PRX.
 DR MGD: MGI:109486; Prdx2.
 DR InterPro: IPR000866; Ahpc-TSA.
 DR Pfam: PF00578; Ahpc-TSA; 1.

SO SEQUENCE 198 AA; 21811 MW; 819F9DD77A70259 CRC64;

Query Match 50.9%; Score 733; DB 11; Length 198;
 Best Local Similarity 69.9%; Pred. No. 2.2e-62;
 Matches 135; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

QY 79 AKISKPAPYEGTAVIDGFEKELKLDYRGKYLVFFFPYPLDFTFVCPTETIAFGDRLEEF 138
 DB 6 AQIGKSPDPFTATAVDAVGAFAKEIKLSYRGKYVLFYPLDFTFVCPTETIAFGDRLEEF 65
 QY 139 RSNITEVAVCSVDSQFTHLAWINTPRROGGLGPIRIPILSDLTHTQISKDYGVLEDSGHT 198
 DB 66 RKLDCGVLVSDSQFTHLAWINTPRKEGGLGPIRIPILSDLTHTQISKDYGVLEDSGHT 125
 QY 199 LRGLFTIIDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETIIP 258
 DB 126 YRGLFTIIDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETIIP 185
 QY 259 DPAGKLYFPDKLN 271
 DB 186 NVDSKEVFSKHN 198

RESULT 8

QY 088376 PRELIMINARY; PRT; 198 AA.
 AC 088376;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Type II peroxiredoxin 1.
 GN PRDX2 OR PRDX1-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RX STRAIN=129SVJ;
 RA MEDLINE=98382588; PubMed=9714804;
 RA Lim M.J., Chae H.Z., Rhee S.G., Yu D.-Y., Lee K.-K., Yeom Y.I.;
 RT "The type II peroxiredoxin gene family of the mouse: molecular
 structure, expression and evolution.";
 RL Gene 216:197-205(1998).
 DR EMBL: AF032722; AAC35744.1; -.
 DR EMBL: AF032718; AAC35744.1; JOINED.
 DR EMBL: AF032719; AAC35744.1; JOINED.
 DR EMBL: AF032720; AAC35744.1; JOINED.
 DR EMBL: AF032721; AAC35744.1; JOINED.
 DR HSSP: P30041; 1PRX.
 DR MGD: MGI:109486; Prdx2.
 DR InterPro: IPR000866; Ahpc-TSA.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 SO SEQUENCE 198 AA; 21791 MW; EEFB0F5426F717AD CRC64;

Query Match 50.5%; Score 727; DB 11; Length 198;
 Best Local Similarity 69.4%; Pred. No. 8.3e-62;
 Matches 134; Conservative 23; Mismatches 36; Indels 0; Gaps 0;

QY 79 AKISKPAPYEGTAVIDGFEKELKLDYRGKYLVFFFPYPLDFTFVCPTETIAFGDRLEEF 138
 DB 6 AQIGKSPDPFTATAVDAVGAFAKEIKLSYRGKYVLFYPLDFTFVCPTETIAFGDRLEEF 65
 QY 139 RSNITEVAVCSVDSQFTHLAWINTPRROGGLGPIRIPILSDLTHTQISKDYGVLEDSGHT 198
 DB 66 RKLDCGVLVSDSQFTHLAWINTPRKEGGLGPIRIPILSDLTHTQISKDYGVLEDSGHT 125
 QY 199 LRGLFTIIDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETIIP 258
 DB 126 YRGLFTIIDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETIIP 185
 QY 259 DPAGKLYFPDKLN 271

Db 186 NVDDSKYFSKH 198

ID	Q9JKY1	PRELIMINARY;	PRT;	199	AA.
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DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Thioresdoxin peroxidase II.
DE Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN-ID 10029;
RA Huang R.N., Lee T.C., Chen Y.C., Tam M.F., Chang K.N.;
RT "Expression of thioresdoxin peroxidase in Chinese hamster ovary
RT cells."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF221841; AAF33369.1; -.
DR HSSP; P30041; 1PRX.
DR InterPro; IPR000866; Ahpc-TSA.
DR Pfam; PF00578; Ahpc-TSA; 1.
KW Peroxidase.
SQ SEQUENCE 199 AA; 22262 MW; CDA6ER015E1A055E CRC64;

Matches 134; Conservative 25; Mismatches 32; Indels 1; Gaps 1;

QY	79	AKISKAPAYMGSTAVI-DGEKELKLNDYRSKYLVFFFFYPDLDFVCPTELIASFGLDEE	137
Dd	6	AKIGYAPAPNEFAYVMDDGQFRDLCISEYRKRYVFFFPYPLDFVCPTETIAFSDAEE	65
QY	138	FRSINTEVVACSVDSOFTHLAMINTPRROGGICPIRIPLSDLTQHOSKDYGVLDESCH	197
Dd	66	FKRLNCQVIGASVDSHCHLAMINTPRKKOGSGCMNIPLYSDPKRTTIAODYGVLAKEDEGI	1253
QY	198	TLRGLFIIDDKGILRQTITLNDLPVGRSVDETLRVLQAFOYTTRKHGEVCPAGMKRGSETII	257
Dd	126	SFRGLFIIDDGILRQTIINDLPVGRSVDETLRVLQAFOFDTRKHGEVCPAGMKRGSDTIK	185
QY	258	PDPAGKLLKPEK 269	
Dd	186	PDVOKSEKEYSK 197	

ID	Q9BG14	PRELIMINARY;	PRT;	199 AA.
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DT 01-JUN-2001 (Tremblrel. 17, created)
DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE Peroxiredoxin 1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Leyens G., Donnay I., Knoops B.,
RT "Cloning of 4 new bovine peroxiredoxins, and screening of the complete
RT peroxiredoxin family in different bovine tissues".
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AF305561; AAG53658.1; -
DR HSSP: P30041; 1PRX.
DR

DR InterPro: IPR000866; Ahpc-TSA.
DR Pfam: PF00578; Ahpc-TSA; 1.
SQ SEQUENCE 199 AA; 22165 MW; BF9926D9F45E01D3 CRC64;

Matches 134; Conservative 23; Mismatches 34; Indels 1; Gaps 1;

QY	79	AKSKAPAYWYGTCVPI -DGEKELKINDYREKUYVFEFFYPIDDFEVCPTETIAFGDNLK 137
Db	6	AKIGRAAQFATAMPDGFKDISLADYKQKVVEFFYPIDDFEVCPTETIAFSDAEE 65
QY	138	FRSINTEVYACSVDSQFPHLAWINTPPROGGLGIPRIPLSDLTHQISKDYGVYLEDSGH 197
Db	66	FKLNCQYIGASVDSHFCFLAWINTPKKQSGGLGPMNIPILSAPKRTIAGDYGVILKADGI 125
QY	138	TLRGLFIIDDKGILRQTLINDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETII 257
Db	126	SFRGLFIIDDKGILRQTLINDLPVGRSVDETLRLVQAFQFDKRGECVCPAGMKPGSDTIK 185
QY	258	PDPAGKLCYFKDK 269
Db	186	PDVQSKSEYFSK 197

ID	093241	PRELIMINARY;	PRT;	199 AA.
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DT      01-NOV-1998 (TrEMBLrel. 08, Created)
DT      01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT      01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE      Natural killer cell enhancing factor (Natural killer enhancing
GN      factor).
GN      NKEF.
OS      Cyprinus carpio (Common carp).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Cyprinus.
OX      NCBL_TaxID=7962;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Shin D., Fujiki K., Nakao M., Yano T.;
RT      "cDNA cloning of a carp homologue of a human natural killer cell
RT      enhancing factor.";
RL      Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Shin D., Fujiki K., Nakao M., Yano T.;
RT      "Organization of the NKEF gene and its expression in the common carp
RT      (Cyprinus carpio).";
RL      Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AB010859; BAA32086.1; -
DR      EMBL; AB048789; BAB39202.1; -
DR      HSSP; P30041; 1PRY
DR      InterPro; IPR000866; AhpC-TSA.
DR      Pfam; PF00578; AhpC-TSA; 1.
SQ      SEQUENCE 199 aa; 22196 MW; 3AB248CE8E99CADA CRC64; .

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Matches 135; Conservative 20; Mismatches 37; Indels 1; Gaps 1;

[illegible]

	RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
	RA	Saito T., Okazaki Y., Gogjohori T., Bono H., Kasukawa T., Saito R.,
	RA	Kadota C., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
	RA	Fleischmann W., Gaasterland T., Gissi C., Ring B., Kochiya H.,
	RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.
	RA	Schirral L.M., Stuhli F., Suzuki R., Tomita M., Wagner L., Washio T.
	RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
	RA	Blake J., Hoffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
	RA	Lyonore P., Marchionni L., Mashima J., Mazzarelli J., Momhaerts P.,
	RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.
	RA	Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitlaker C., Wilming L.
	RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
	RA	Hayashizaki Y.;
	RT	"Functional annotation of a full-length mouse cDNA collection.";
	RL	Nature 409:685-690(2001).
	DR	EMBL: AK010688; BABZ7120.1; --
	DR	HSSP: P30041; IPRX.
	DR	MGD: MGI:99523; Prdx1.
	DR	InterPro: IPR000866; Anpc-TSA.
	DR	Pfam: PF00578; Ahpc-TSA.1
	SO	SEQUENCE 199 AA; 22236 MW; BEF5C989D86124D1 CRC64;
	Query Match	49.9%; Score 718.5; DB 11; Length 199;
	Best Local Similarity	68.8%; Pred. No. 5,5e-61;
	Matches 132; Conservative 27; Mismatches 32; Indels 1; Caps	
OY	79	AIISKRPAPWEETANI-DGEFKELKLTIRGKYLVFFYPIDTFVPCPTETIARGLREE 133
DB	6	AAIGYPAPEFKATVAMPDGQFDISLSEKKYVVFEPYPIDFPFVCPTEIIAFSDADE 65
OY	138	FSRINTEVACVSQSOFTHLAMINTPRROGGAGLPRIPLSDLHNSKDYGVYLEDSGH 197
DB	66	EKLKNCQVITGASVDSHFCHLAMINTPKKGSLGPNIPILSDPKRRITIAODGVLLKADEGI 125
OY	198	TURLGFIIDDGKILRQTILNDLPVGRSVDETLRILVOAFOYTDKNGEVCAPMGKPGSETII 257
DB	126	SFRGLEFIIDDGKILRQTINDLPVGRSVDIELIRLVQAOFQPDKNGEVCAPMGRKGSPTIK 185
OY	258	PDPACKLKPYDK 269
DB	186	PDVAKSKKEYFER 197
RESULT 14		
OSDBA9		
ID	09DBA9	PRELIMITARY; PRT: 198 AA.
DT	09DBA9	
DC	01-JUN-2001 (TREMBlrel. 17, Created)	
DD	01-JUN-2001 (TREMBlrel. 17, Last sequence update)	
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)	
DE	Peroxiredoxin 2.	
CN	PRDX2.	
OC	Mus musculus (Mouse).	
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
CC	Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.	
OX	[NCBI_TaxID=10099];	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6J; TISSUE=CEREBELLUM;	
RC	MEDLINE=21085660; Pubmed=11217851;	
RA	Kawai J., Shigaawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,	
RA	Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,	
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,	
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,	
RA	Kadota C., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,	
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,	
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.	
RA	Schirral L.M., Stuhli F., Suzuki R., Tomita M., Wagner L., Washio T.,	
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,	
RA	Blake J., Hoffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,	

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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:15:02 ; Search time 11 Seconds

(without alignments)
1021.826 million cell updates/sec

Title: US-09-911-346-2
Perfect score: 1441
Sequence: 1 MEALPLLAATTPDGHRRRL.....GSEFTIPDPAGKLKPEDKLN 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1441	100.0	271	PDX4_HUMAN	Q13162 homo sapien
2	1296	89.9	274	PDX4_BOVIN	Q9bg12 bos taurus
3	1262.5	87.6	274	PDX4_MOUSE	O08807 mus musculus
4	749	52.0	199	PDX2_BOVIN	Q9bg13 bos taurus
5	746	51.8	198	PDX2_HUMAN	P22119 homo sapien
6	744	51.6	198	PDX2_RAT	P35704 rat mus musculus
7	735.5	51.0	199	PDX1_HUMAN	Q06830 homo sapien
8	732	50.8	198	PDX1_MOUSE	O61171 mus musculus
9	731.5	50.8	200	PDX1_MOUSE	O61171 mus musculus
10	730.5	50.7	199	PDX1_MOUSE	O63716 rat mus musculus
11	721.5	50.1	199	PDX1_MOUSE	P35700 mus musculus
12	703	48.8	256	PDX3_HUMAN	P30048 homo sapien
13	691	48.0	257	PDX3_BOVIN	P35703 bos taurus
14	689	47.8	257	PDX3_MOUSE	P20108 mus musculus
15	667	46.3	199	PDX2_BRUMA	Q17172 brugia mala
16	660	45.8	200	PDX1_MOUSE	O91191 oncorhynchus
17	639.5	44.4	226	PDX1_MOUSE	Q21824 caenorhabdi
18	631.5	43.8	199	PDX1_MOUSE	Q26935 trypanosoma
19	592.5	41.1	210	PDX1_MOUSE	Q26935 trypanosoma
20	589	40.9	196	PDX1_MOUSE	Q26935 trypanosoma
21	588.5	40.8	210	PDX1_MOUSE	Q26935 trypanosoma
22	584	40.5	195	PDX1_MOUSE	Q26935 trypanosoma
23	582.5	40.4	265	PDX1_MOUSE	Q26935 trypanosoma
24	571	39.6	266	PDX1_MOUSE	Q26935 trypanosoma
25	570.5	39.6	200	PDX1_MOUSE	Q26935 trypanosoma
26	567	39.3	195	PDX1_MOUSE	Q26935 trypanosoma
27	561	38.9	229	PDX1_MOUSE	Q26935 trypanosoma
28	556.5	38.6	229	PDX1_MOUSE	Q26935 trypanosoma
29	548	38.0	199	PDX1_MOUSE	Q26935 trypanosoma
30	489	33.9	127	PDX2_MOUSE	P51272 porphyra pu
31	479.5	33.3	233	PDX2_MOUSE	P19476 entamoeba h
32	477	33.1	178	PDX2_MOUSE	P23161 clostridium
33	404	28.0	198	PDX2_MOUSE	P56876 helicobacte

34	403	28.0	198	1	TSA_HUMAN	P21762 helicobacte
35	398.5	27.7	197	1	TSA_BUCAL	P57279 buchnera ap
36	394.5	27.4	204	1	VC42_ODOSI	P49537 odontella s
37	341	23.7	222	1	TDH_XAQUE	O67024 aquilex aeo
38	332	23.0	186	1	AHPC_ECOLI	P26427 escherichia
39	327	22.7	186	1	AHPC_SALTY	P19479 salmonella
40	318.5	22.1	215	1	TDH_XTHMA	O9wz14 thermotoga
41	316.5	22.0	199	1	TDH2_THMAC	O9h113 thermoplas
42	310.5	21.5	217	1	TDH_XMETHA	O58146 methanococ
43	308	21.4	215	1	TDH_XSULSO	P35895 sulfolobus
44	302	21.0	187	1	AHPC_BACSU	P80239 bacillus su
45	291.5	20.2	215	1	TDH_XARCFU	O29969 archaeoglob

ALIGNMENTS

RESULT 1	ID	PDH4_HUMAN	STANDARD:	PRT:	271 AA.
AC	Q13162	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998	(Rel. 36, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Peroxisomal oxidase 4 (EC 1.11.1.-) (Prx-IV) (Thioredoxin peroxidase A0372)				
DE	(Thioredoxin-dependent peroxidase A0372) (Antioxidant enzyme A0372)				
DE	AOE372) (AOE37-2).				
GN	PDX4.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID:9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE:98049564; PubMed:9388242;				
RT	Jin D.-Y., Chae H.Z., Rhee S.G., Jeang K.-T.;				
RT	"Regulatory role for a novel human thioredoxin peroxidase in NF-kappa				
RT	B activation."				
RL	J. Biol. Chem. 272:30952-30961(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RP	TISSUE:Brain;				
RA	Strausberg R.;				
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	OVEROXIDATION OF CYS-124.				
RA	Rabilloud T.;				
RL	Unpublished observations (JUL-2002).				
CC	-1- FUNCTION: Probably involved in redox regulation of the cell.				
CC	modulation of NF-kappa-B in the cytosol by a				
CC	regulation of NF-kappa-B-alpha phosphorylation.				
CC	-1- SUBUNIT: Homodimer or heterodimer with PDX1; disulfide-linked,				
CC	upon oxidation (By similarity).				
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.				
CC	-1- MISCELLANEOUS: The active site is the redox-active Cys-124				
CC	oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-245-SH of the				
CC	other subunit to form an intermolecular disulfide with a				
CC	concomitant homodimer formation. The enzyme may be subsequently				
CC	regenerated by reduction of the disulfide by thioredoxin.				
CC	-1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-				
CC	124 (to Cys-SO3H) upon oxidative stress.				
CC	-1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.				
CC	-----				
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CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: U25182; AAB95175.1; -				
DR	EMBL: BC003609; AAH03609.1; -				

DR EMBL: BC007107; AAH07107.1; -;
 DR EMBL: BC016770; AAH16770.1; -;
 DR HSSP: P30041; 1PRX.
 DR Genew: HGNC:17169; PRDX4.
 DR MIM: 606506; -;
 DR InterPro: IPR000866; Ahpc-TSA.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.
 CC DOMAIN 20 30
 FT ACT SITE 124 124 POLY-LEU.
 FT DISULFID 124 245 REDOX-ACTIVE.
 SQ SEQUENCE 271 AA: 30540 MW: 7556580049PC60F CRC64;

Query Match 100.0%; Score 1441; DB 1; Length 271;
 Best Local Similarity 100.0%; Pred. No. 4.7e-126;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEALPLAATTPDHGRRLRLPLFLPAGAVQGWTEPERTRTEECHEFTAGGQVY 60
 DB 1 MEALPLAATTPDHGRRLRLPLFLPAGAVQGWTEPERTRTEECHEFTAGGQVY 60
 QY 61 PGEASRVADSHLSLAKISKAPYMEGTAVIDGFEKELTDYRGKYLVEFFYPLDF 120
 DB 61 PGEASRVADSHLSLAKISKAPYMEGTAVIDGFEKELTDYRGKYLVEFFYPLDF 120
 QY 121 TFCVPTETIAFGDRLEEFERSINTEVACSVDSQFTHLAMINTPRROGSLGPIRLPLSDL 180
 DB 121 TFCVPTETIAFGDRLEEFERSINTEVACSVDSQFTHLAMINTPRROGSLGPIRLPLSDL 180
 QY 181 THQISKRYGYLEDSGHTLGLFTIDDKGILRQITLNDLPVGRSVDETLRLVOAFQYTDK 240
 DB 181 THQISKRYGYLEDSGHTLGLFTIDDKGILRQITLNDLPVGRSVDETLRLVOAFQYTDK 240
 QY 241 HGEVCPAGMKPGSETIIPDPAGKLYFDKLN 271
 DB 241 HGEVCPAGMKPGSETIIPDPAGKLYFDKLN 271

RESULT 2

PDX4_BOVIN STANDARD; PRT; 274 AA.

AC 09BGIZ;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Peroxiredoxin 4 (EC 1.11.1.1) (Prx-IV).
 GN PRDX4.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Leyens G., Donnay I., Knoops B.;
 RT "Cloning of 4 new bovine-peroxiredoxins, and screening of the complete
 RT peroxiredoxin family in different bovine tissues.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Probably involved in redox regulation of the cell.
 CC Regulates the activation of NF-kappa-B in the cytosol by a
 CC modulation of I-kappa-B-alpha phosphorylation (By similarity).
 CC -1- SUBUNIT: Homodimer or heterodimer with PRDX1; disulfide-linked,
 CC upon oxidation (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- MISCELLANEOUS: The active site is the redox-active Cys-127
 CC oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-248-SH of the
 CC other subunit to form an intermolecular disulfide with a
 CC concomitant homodimer formation. The enzyme may be subsequently
 CC regenerated by reduction of the disulfide by thioredoxin (By
 CC similarity).
 CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-
 CC 127 (to Cys-SO3H) upon oxidative stress (By similarity).

CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.

CC -----
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 CC or send an email to license@isb-sib.ch).

DR EMBL: AF305563; AAC53660.1; -;
 DR HSSP: P30041; 1PRX.
 DR InterPro: IPR000866; Ahpc-TSA.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.
 CC ACT SITE 127 127 REDOX-ACTIVE.
 FT DISULFID 127 248 INTERCHAIN (PARTIAL) (BY SIMILARITY).
 SQ SEQUENCE 274 AA: 30741 MW: AE141766FC170E37 CRC64;

Query Match 89.9%; Score 1296; DB 1; Length 274;
 Best Local Similarity 92.1%; Pred. No. 1.3e-112;
 Matches 246; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 5 PLAAATPDHGRRLRLPLFLPAGAVQGWTEPERTRTEECHEFTAGGQVYGEA 64
 DB 8 PLPATTIAPGRSRKLLPLFLFLRAEAVKGEAEERPTREECHFYAGGQVYGEV 67
 QY 65 SRVSVADSHLSLAKISKAPYMEGTAVIDGFEKELTDYRGKYLVEFFYPLDFEVC 124
 DB 68 SRVSVADSHLSLAKISKAPYMEGTAVIDGFEKELTDYRGKYLVEFFYPLDFEVC 127
 QY 125 PTEIIAFGRDRLEEFERSINTEVACSVDSQFTHLAMINTPRROGSLGPIRLPLSDLTHQI 184
 DB 128 PTEIIAFGRDRLEEFERSINTEVACSVDSQFTHLAMINTPRROGSLGGINIPPLADLNHQI 187
 QY 185 SKDGYVLEDSGHTLRGLFTIDDKGILRQITLNDLPVGRSVDETLRLVOAFQYTDKGEV 244
 DB 188 SKDGYVLEDSGHTLRGLFTIDDKGILRQITLNDLPVGRSVDETLRLVOAFQYTDKGEV 247
 QY 245 CPAGMKPGSETIIPDPAGKLYFDKLN 271
 DB 248 CPAGMKPGSETIIPDPAGKLYFDKLN 274

RESULT 3

PDX4_MOUSE STANDARD; PRT; 274 AA.

AC 008807;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Peroxiredoxin 4 (EC 1.11.1.1) (Prx-IV) (Thioredoxin peroxidase A0372)
 DE (Thioredoxin-dependent peroxidase A0372) (Antioxidant enzyme
 DE AOE372).
 GN PRDX4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=21121079; Pubmed=11229364;
 RA Wong C.M., Chun A.C., Kok K.H., Zhou Y., Fung P.C., Kung H.F.,
 RA Jiang K.-T., Jin D.-Y.;
 RT "Characterization of human and mouse peroxiredoxin IV: evidence for
 RT inhibition by Prx-IV of epidermal growth factor- and p53-induced
 RT reactive oxygen species.";
 RL Antioxid. Redox. Signal. 2:507-518(2000).
 CC -1- FUNCTION: Probably involved in redox regulation of the cell.
 CC Regulates the activation of NF-kappa-B in the cytosol by a
 CC modulation of I-kappa-B-alpha phosphorylation.
 CC -1- SUBUNIT: Homodimer or heterodimer with PRDX1; disulfide-linked,

CC Leyvens G., Donnay I., Knoops B.;
RT "Cloning of a new bovine peroxidoxin, and screening of the complete
RT peroxidoxin family in different bovine tissues.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Involved in redox regulation of the cell. Reduces
CC peroxides with reducing equivalents provided through the
CC thioredoxin system. It is not able to receive electrons from
CC glutaredoxin. May play an important role in eliminating peroxides
CC generated during metabolism. Might participate in the signaling
CC cascades of growth factors and tumor necrosis factor- α by
CC regulating the intracellular concentrations of H2O(2).
CC -1- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- MISCELLANEOUS: The active site is the redox-active Cys-52 oxidized
CC to Cys-SOH. Cys-SOH rapidly reacts with Cys-173-SH of the other
CC subunit to form an intermolecular disulfide with a concomitant
CC homodimer formation. The enzyme may be subsequently regenerated by
CC reduction of the disulfide by thioredoxin (By similarity).
CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-
CC 52 (to Cys-SO3H) upon oxidative stress (By similarity).
CC -1- SIMILARITY: BELONGS TO THE AHP/C/TA FAMILY.
CC -----
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58 GVDPGPAEDVIGANDUETPIGSAVETGRDIDVECHMVTTCGEEVETPTETVNDGCTVITMNNR 117

61 QYFGEASRVSYADHSLHLSSKAKISKAPYWECTAVIINGEKFELKLTIDYRGKILYVEFP 120

Db 121 LDFTVCPTEIIAAGDRIIEFKSINTEVYACSDSOETHLAWINTPROGGIGPIRIPDL 180

Db 181 S D L N H Q I S K D Y G Y L E D S G H T L R G L F T I D D K G V L R Q T L N D E P V G R S V D E T L R L V Q A R F Y 240

Oy	238	TDKHGEVCPAGNMPGSEIIPDPAGKLELYFDKN	271
Db	241	TDKHGEVCPAGNMPGSEIIPDPAGKLELYFDKN	274

RESULT 4
PDX2_BOVIN

AC 09B2JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 JT 15-JUN-2002 (Rel. 41, Last sequence update)

DR 15-JUN-2002 (Rel. 41, last annotation update)
 DE Peroxiredoxin 2 (EC 1.11.1.-).
 GN PRDX2.
 OS Bos taurus (Bovine).
 OS Bos taurus (Bovine).

0C Eukarya; Metazoa; Chordata; Craniata; Euteleostomi;
0C Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
0C Bovidae; Bovinae; Bos.
NC01:taxid=9913

RN (1) _____
 BP SEQUENCE FROM N.A.
 RC TISSUE-Liver;

CC Leyvens G., Donnay I., Knoops B.;
RT "Cloning of a new bovine peroxidoxin, and screening of the complete
RT peroxidoxin family in different bovine tissues.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Involved in redox regulation of the cell. Reduces
CC peroxides with reducing equivalents provided through the
CC thioredoxin system. It is not able to receive electrons from
CC glutaredoxin. May play an important role in eliminating peroxides
CC generated during metabolism. Might participate in the signaling
CC cascades of growth factors and tumor necrosis factor- α by
CC regulating the intracellular concentrations of H2O(2).
CC -1- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- MISCELLANEOUS: The active site is the redox-active Cys-52 oxidized
CC to Cys-SOH. Cys-SOH rapidly reacts with Cys-173-SH of the other
CC subunit to form an intermolecular disulfide with a concomitant
CC homodimer formation. The enzyme may be subsequently regenerated by
CC reduction of the disulfide by thioredoxin (By similarity).
CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-
CC 52 (to Cys-SO3H) upon oxidative stress (By similarity).
CC -1- SIMILARITY: BELONGS TO THE AHP/C/TA FAMILY.
CC -----
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DR EMBL: AF305562; AAG53659.1; -.
DR HSSP: P30041; 1PRX.
DR InterPro: IPR000866; AhpC-TSA.
DR

KM	Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.
FT	ACT_SITE 52 REDOX-ACTIVE (BY SIMILARITY).
FT	DISULFID 52 173 INTERCHAIN (PARTIAL) (BY SIMILARITY).
SD	SEQUENCE 199 AA; 21946 MW; 5F25CCE54090E2DE CRC64;

Query Match	52.0%	Score 749	DB 1	Length 199
Best Local Similarity	69.1%	Pred. No. 3	6e-62	
Matches 134	Conservative 26	Mismatches 34	Indels 0	Gaps 0

[illegible]

OY 138 FRSINTEVVACSVDSOETHLAMIINTPRROGGGLPIRIPILSDUTHIOISKDYGVYLLEDSGH 197
 | : ||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
66 EUKI NENVI CYSVDSEOTTHI VUININPPEKCECTCDPTDNDT DTPPPSCKVIT KZECT 105

[illegible]

258 PDPAGRIKXFDDKLN 271
| : : | | |

DD 186 PNVDSKEYSKHN 199 .
RESULT 5

	PDX2_HUMAN	STANDARD:	PRT:	198 AA.
ID	PDX2_HUMAN			
AC	P32119: P31945: Q92763;			
DE	01-OCF-1903 (P01327_C903504)			

DT 01-NOV-1997 (Rel. 35, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Peroxiredoxin 2 (EC 1.11.1.-) (Thioredoxin peroxidase 1) (Thioredoxin-

DE Penicillin-Biotinylated Leukocyte 1 (inter specific anti-oxidant protein)
TS(A) (PRP) (Natural Killer cell enhancing factor B) (NKEF-B).
GS PRDX2 OR TDPXI OR NKEFB.
NS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94193012; PubMed=8144038;
RT Lim Y.-S., Cha M.-K., Kim H.-K., Kim I.-H.;
RA "The thiol-specific antioxidant protein from human brain: gene
cloning and analysis of conserved cysteine regions.";
RL Gene 140:279-284(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94299283; PubMed=8026862;
RA Shau H., Butterfield L.H., Chiu R., Kim A.;
RT "Cloning and sequence analysis of candidate human natural killer-
enhancing factor genes.";
RL Immunogenetics 40:129-134(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RT Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 35-198 FROM N.A.
RA Oberbauer I.;
RT Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE OF 17-25; 140-150 AND 163-185.
RC TISSUE=Keratinocytes;
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969(1992).
RN [6]
RP SEQUENCE OF 17-26 AND 93-103.
RC TISSUE=Erythrocyte;
RX MEDLINE=94147970; PubMed=8313871;
RA Goletz O., Hughes G.J., Futiger S., Paquet N., Bairoch A.,
Paquelin C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,
Balant L., Hochstrasser D.F.;
RT "Plasma and red blood cell protein maps: update 1993.";
RL Electrophoresis 14:1223-1231(1993).
RN [7]
RP SEQUENCE OF 17-26; 111-135 AND 140-157.
RC TISSUE=Colon carcinoma;
RX MEDLINE=97295306; PubMed=9150948;
RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
RT "A two-dimensional gel database of human colon carcinoma proteins.";
RL Electrophoresis 18:605-613(1997).
RN [8]
RP OVEROXIDATION OF CYS-51.
RX PubMed=11904290;
RA Rabilloud T., Heller M., Gasnier F., Luche S., Rey C., Aebersold R.,
Benhammed M., Lissot P., Linnard J.;
RT "Proteomic analysis of cellular response to oxidative stress.
Evidence for in vivo overoxidation of peroxiredoxins at their active
site.";
RL J. Biol. Chem. 277:19396-19401(2002).
RN [9]
RP FUNCTION: Involved in redox regulation of the cell. Reduces
peroxides with reducing equivalents provided through the
thioredoxin system. It is not able to receive electrons from
glutaredoxin. May play an important role in eliminating peroxides
generated during metabolism. Might participate in the signaling
cascades of growth factors and tumor necrosis factor-alpha by
regulating the intracellular concentrations of H2(2)O(2).
RN [10]
RP FUNCTION: Enhances natural killer (NK) cells activity.
RN [11]
RP SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By
similarity).
RN [12]
RP SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MISCELLANEOUS: The active site is the redox-active Cys-51 oxidized

CC	to Cys-SOH. Cys-SOH rapidly reacts with Cys-172-SH of the other
CC	submit to form an intermolecular disulfide with a concomitant
CC	homodimer formation. The enzyme may be subsequently regenerated by
CC	reduction of the disulfide by thioredoxin.
CC	-1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-
CC	51 (to Cys-SO ₃ H) upon oxidative stress.
CC	-1- SIMILARITY: BELONGS TO THE AHPc/TSA FAMILY.
CC	-----
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CC	or send an email to license@1sb-sib.ch).
CC	-----
DR	EMBL; Z22548; CAA80269.1; -
DR	EMBL; L19185; AAA50465.1; -
DR	EMBL; BC000452; AAA00452.1; -
DR	EMBL; BC003022; CAA03022.1; -
DR	EMBL; X82321; CAA57764.1; -
DR	HSP; P30041; 1PRX
DR	SWISS-2DPAGE; P32119; HUMAN.
DR	Aarhus/Ghent-2DPAGE; G116; IEF.
DR	Genew; HGNC:9353; PRDX2.
DR	MIM; 600538; -
DR	InterPro: IPR00866; AHPc-TSA.
DR	Pfam: PF00578; AHPc-TSA; 1.
KW	Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.
KW	Act_Site 51 51
FT	DISULFID 51 172
FT	CONFLICT 59 66
FT	CONFLICT 82 82
FT	CONFLICT 105 105
FT	CONFLICT 120 120
FT	CONFLICT 175 175
FT	CONFLICT 180 180
Q	SEQUENCE 198 AA; 21892 MW; 1AC781D908B32B46 CRC64;
	INTERCHAIN (PARTIAL) (BY SIMILARITY).
	SNRAEDR -> TTVKRTSA (IN REF. 1).
	T -> N (IN REF. 2).
	A -> G (IN REF. 2).
	T -> N (IN REF. 1).
	G -> A (IN REF. 1).
	S -> R (IN REF. 1).

	Query March Similarity	51.8%;	Score 746;	DB 1;	Length 198;
	Best Local Similarity	70.5%;	Pred. No. 6,9e-62;		
	Matches 136;	Conservative	26;	Mismatches 31;	Indels 0;
					Gaps 0;
QY	79	AKISPAPEWEGTAVIDGEEFKELKLTIDYRGKYLVEFFYPILDFTEVCPTETIIAFGDRLEEF	138		
Db	6	ARIGKPADPFAKATAVNDGAFKEVKLSIDYKGYVLFEPILDFTEVCPTETIIAFSRAEDF	65		
QY	139	RSINTEWVACVDSQFTHLAININTPRRGGIGLPIRIPILSLUTHQISNDYGVLEDSGHT	198		
Db	66	RKICEVVLGVSVDSQFTHLAININTPRKGGIGLPINIPILLAVTRLSBDYVLKTDGEGIA	125		
QY	199	LRGFIIDDKSILKQITLNDLPVGRSVDETLRLVQAFQYTKHKGECVAGKPGSETIIP	258		
Db	126	YRGFIIDGKSVLQIITYNDLPVGRSVDEALRLVQAFQYTDHGEVCPAGKPGSDTIKP	185		
QY	259	DPAGKLYFDKLN	271		
Db	186	NVDSKEVFSKHN	198		
RESULT	6				
PDX2_RAT					
ID	PDX2_RAT	STANDARD;	PRT;	198	AA.
AC	p35704;				
DT	01-JUN-1994 (Rel. 29, Created)				
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Peroxiredoxin 2 (EC 1.11.1.-) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxidase reductase 1) (Thiol-specific antioxidant protein) (TSA).				
DE	(TSA).				
GN	PRDX2 OR TDPX1.				
OS	Rattus norvegicus (Rat).				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ratus.
 ON NCB1_TaxID=10116;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=9431629; PubMed=8041738;
 RA Chae H.Z., Robison K., Poole L.B., Church G., Storz G., Rhee S.G.;
 RT "Cloning and sequencing of thiol-specific antioxidant from mammalian
 brain: alkyl hydroperoxide reductase and thiol-specific antioxidant
 define a large family of antioxidant enzymes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:7017-7021(1994).
 CC -1- FUNCTION: Involved in redox regulation of the cell. Reduces
 peroxides with reducing equivalents provided through the
 thioredoxin system. It is not able to receive electrons from
 glutaredoxin. May play an important role in eliminating peroxides
 generated during metabolism. Might participate in the signaling
 cascades of growth factors and tumor necrosis factor-alpha by
 regulating the intracellular concentrations of H(2)O(2).
 CC -1- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By
 similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- MISCELLANEOUS: The active site is the redox-active Cys-51 oxidized
 to Cys-SOH. Cys-SOH rapidly reacts with Cys-172-SH of the other
 subunit to form an intermolecular disulfide with a concomitant
 homodimer formation. The enzyme may be subsequently regenerated by
 reduction of the disulfide by thioredoxin (By similarity).
 CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-
 51 (to Cys-SO3H) upon oxidative stress (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE AHPc/TSA FAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U06099; AAA19959.1; -;
 DR HSSP: P30041; IPRX.
 DR InterPro: IPR000866; AHPc-TSA.
 DR Pfam: PF00578; AHPc-TSA; 1.
 KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.
 FT ACT_SITE 51 51 REDOX-ACTIVE (BY SIMILARITY).
 FT DISULFID 51 172 INTERCHAIN (PARTIAL) (BY SIMILARITY).
 FT SEQUENCE 198 AA; 21784 MW; FC6ADB0B9C447B CRC64;
 SO
 Query Match 51.6%; Score 744; DB 1; Length 198;
 Best Local Similarity 71.0%; Pred. No. 1,1e-61;
 Matches 137; Conservative 22; Mismatches 34; Indels 0; Gaps 0;

DR 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Peroxiredoxin 1 (EC 1.11.1.-) (Thioredoxin peroxidase 2) (Thioredoxin-
 dependent peroxidase reductase 2) (Proliferation-associated protein PAG)
 DE (Natural killer cell enhancing factor A) (NKEF-A).
 GN PDx1 OR TDPx2 OR PAGB OR PAGA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ON NCB1_TaxID=9606;
 RX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9326652; PubMed=8496166;
 RA Prosperi M.T., Terbus D., Karczinski I., Goubin G.;
 RT "A human cDNA corresponding to a gene overexpressed during cell
 proliferation encodes a product sharing homology with amoebic and
 bacterial proteins.";
 RL J. Biol. Chem. 268:11050-11056(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94299283; PubMed=8026862;
 RA Shu H., Butterfield L.H., Chiu R., Kim A.;
 RT "Cloning and sequence analysis of candidate human natural killer-
 enhancing factor genes.";
 RL Immunogenetics 40:129-134(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Urinary bladder;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP OVEROXIDATION OF CYS-52.
 RA Rabilloud T.;
 RL Unpublished observations (JUL-2002).
 CC -1- FUNCTION: Involved in redox regulation of the cell. Reduces
 peroxides with reducing equivalents provided through the
 thioredoxin system but not from glutaredoxin. May play an
 important role in eliminating peroxides generated during
 metabolism. Might participate in the signaling cascades of growth
 factors and tumor necrosis factor-alpha by regulating the
 intracellular concentrations of H(2)O(2).
 CC -1- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By
 similarity). May form heterodimers with AOR2.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- INDUCTION: Constitutively expressed in most human cells; is
 induced to higher levels upon serum stimulation in untransformed
 and transformed cells.
 CC -1- MISCELLANEOUS: The active site is the redox-active Cys-52 oxidized
 to Cys-SOH. Cys-SOH rapidly reacts with Cys-173-SH of the other
 subunit to form an intermolecular disulfide with a concomitant
 homodimer formation. The enzyme may be subsequently regenerated by
 reduction of the disulfide by thioredoxin.
 CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-
 52 (to Cys-SO3H) upon oxidative stress.
 CC -1- SIMILARITY: BELONGS TO THE AHPc/TSA FAMILY.
 CC -1- DATABASE: NAME=Atlas Genet. Cyto genet. Oncol. Haematol.;
 WWW="http://www.inbioogen.fr/services/chromocancer/genes/PAGID266.html".
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X67951; CAA48137.1; -;
 DR EMBL: L19184; AAA50464.1; -;
 DR EMBL: BC007063; AAH07063.1; -;
 DR EMBL: BC021683; AAH21683.1; -;
 DR PIR: S32099; S32099.
 DR PIR: A46711; A46711.
 DR HSSP: P30041; IPRX.

CC		generated during metabolism Might participate in the signaling cascades of growth factors and tumor necrosis factor- α by regulating the intracellular concentrations of H ₂ O(2).
CC	-1-	SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By similarity).
CC	-1-	SUBCELLULAR LOCATION: Cytoplasmic.
CC	-1-	TISSUE SPECIFICITY: Widely expressed with highest levels in bone marrow. High levels also found in heart, brain, kidney and skeletal muscle. Lower levels in liver, lung and thymus.
CC	-1-	MISCELLANEOUS: The active site is the redox-active Cys-51 oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-172-SH of the other subunit to form an intermolecular disulfide with a concomitant homodimer formation. The enzyme may be subsequently regenerated by reduction of the disulfide by thioredoxin (By similarity).
CC	-1-	MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-51 (to Cys-SO ₃ H) upon oxidative stress (By similarity).
CC	-1-	SIMILARITY: BELONGS TO THE AHPc/TSA FAMILY.
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or-send-an-email-to-license@isb-sib.ch).
CC		-----
DR	EMBL:	U51679; AAB01941.1; -
DR	EMBL:	X82067; CAA57566.1; -
DR	EMBL:	U20611; AAA69475.1; -
DR	HSSP:	P30041; IPRX.
DR	SWISS-2DPAGE:	Q61171; MOUSE.
DR	MGD:	MGI:109486; Ptdx2.
DR	InterPro:	IPR000866; Ahpc-TSA.
DR	Pfam:	PF00578; Ahpc-TSA; 1.
KM	Amino acid:	Peroxidase; Oxidoreductase; Redox-active center.
FT	ACT_SITE	51 51
FT	DISULFID	51 172
FT	CONFLICT	97 97 INTERCHAIN (PARTIAL) (BY SIMILARITY).
FT	CONFLICT	182 182 G->A (IN REF. 3).
FT	CONFLICT	182 182 T->N (IN REF. 3).
SO	SEQUENCE	198 AA; 21778 MW; FE216F5426F717AD CRC64;
	Query Match	50.8%; Score 732; DB 1; Length 198;
	Best Local Similarity	69.9%; Pred. No. 1,4e-60;
	Matches 133; Conservative	23; Mismatches 35; Indels 0; Gaps 0;
QY	79 AKISKAPVWEGTAIVDIGEKEKLTLDYRGKYLVFFFPDLPFEVCPTETIIAFSDRLREEF	138
Db	6 AQICKSAPDFATNAVVGAGFAEKIKLSYRGKVVLFEPPLDFTEVCPTETIIAFSDHAEDF	65
QY	139 RSINTEVAVACVSQSOFTHLAININFRROGGLGPIRIPLSLDTLHQISKDGVYLEDSGHT	198
Db	66 RKLCCEVLGVSVDSQFTHLAININFRREGGGGLPINIPLADVTKSLSONYGVLANDEGIA	125
QY	199 LRGEFIIDDKGLIGLOITLNDLPVGRSVDELRLVOAQCYTPKHGEVCPAGKPSSERTIP	258
Db	126 YRGFEIIDAGVGLKQITIVNDLPVGRSVDEALRLVOAFQYTDHEBECVPAWGPKPSDITKP	185
QY	259 DPAGCKLYFDKLN 271	
Db	186 NVDDSKREYFSKN 198	
	RESULT 9	
	TDX_CYNPY	
AC	TDX_CYNPY STANDARD; PRT; 200 AA.	
DT	01-NOV-1997 (Rel. 35, Created)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	Thioredoxin peroxidase (thioredoxin-dependent peroxide reductase)	
DE	(Animal blastomere protein, 25 kDa) (ARP-25).	
CC	Cynops pyrrhogaster (Japanese common newt).	
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	

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CC Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Embryo;
RC Tabata T., Kamio K., Tajima T., Kaneda T., Suzuki A.;
RT "Pag gene-like protein (ABP-25) of Cynops embryo: regional
RL distribution and gene expression during early embryogenesis.";
RL Roux's Arch. Dev. Biol. 204:400-405(1995).
CC
CC -1- FUNCTION: REDUCES PEROXIDES WITH REDUCING EQUIVALENTS PROVIDED
CC THROUGH THE THIOREDOXIN SYSTEM. IT IS NOT ABLE TO RECEIVE
CC ELECTRONS FROM GLUTAREDOXIN. MAY PLAY AN IMPORTANT ROLE IN
CC ELIMINATING PEROXIDES GENERATED DURING METABOLISM. MIGHT
CC PARTICIPATE IN THE SIGNALING CASCADES OF GROWTH FACTORS AND TUMOR
CC NECROSIS FACTOR-ALPHA BY REGULATING THE INTRACELLULAR
CC CONCENTRATIONS OF H(2)O(2) (BY SIMILARITY).
CC
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED, UPON OXIDATION (BY
CC SIMILARITY).
CC
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC
CC -1- PTM: THE CYS-52-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
CC H(2)O(2), AND THE OXIDIZED CYS-52 (PROBABLY CYS-SOH) RAPIDLY
CC REACTS WITH CYS-173-SH OF THE OTHER SUBUNIT TO FORM AN
CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE
CC REDUCED BY THIOREDOXIN (BY SIMILARITY).
CC
CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
CC
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CC
CC
CC DR EMBL; D37808; BAA07054.1; -.
CC DR HSSP; P30041; 1PRX.
CC DR InterPro: IPR000866; AHPc-TSA.
CC DR Pfam: PF00578; AHPc-TSA; 1.
CC KW Antioxidant.
CC FT ACT_SITE 52 52 BY SIMILARITY.
CC FT ACT_SITE 173 173 BY SIMILARITY.
CC FT ACT_SITE 200 AA; 22339 MW; 55A2B0801D633990 CRC64;
CC SQ
CC
CC Query Match 50.8%; Score 731.5; DB 1; Length 200;
CC Best Local Similarity 71.5%; Pred. No. 1.5e-60;
CC Matches 138; Conservative 22; Mismatches 32; Indels 1; Gaps 1;
CC
CC QY 78 KAKISPAPEWEGTAVI-DGEFKELKLDYRGKLVFFFPYLDFTFVCPTEIIAFGRLE 136
CC Db 5 KAOIGKPAPEFOAKAVMGEGFEKIKLDYRGKLVFFFPYLDFTFVCPTEIIAFGRLE 64
CC
CC QY 137 EFRSINTEVAVCSVDSTHLAMINTPRROGGLGPIRIPILSDLRHQISKDYGVLDESG 196
CC Db 65 EFRKINCLIASVDSHCHLAWINTSRKSGLSMKIPLVADTRRTISODYGLAKEDEG 124
CC
CC QY 197 HLRGLFTIIDDKGLRQITLNDLPVGRSVDETLRLVQAFQYDKHGEVCPAGKRGSESTI 256
CC Db 125 ISFRGLFTIIDDKGLRQITLNDLPVGRSVDETLRLVQAFQYDKHGEVCPAGKRGSESTI 184
CC
CC QY 257 ITPDPAKLYFDK 269
CC Db 185 KPDISKSEYFSK 197
CC
CC RESULT 10
CC PDX1_RAT
CC ID PDX1_RAT STANDARD; PRT; 199 AA.
CC AC Q63716;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Peroxiredoxin 1 (EC 1.11.1.-) (Thioredoxin peroxidase 2) (Thioredoxin-
CC dependent peroxidase reductase 2) (Heme-binding 23 kDa protein) (HBP23).

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GN PROX1 OR TDPX2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley; TISSUE=Liver;
RC MEDLINE=96027454; PubMed=7577926;
RX Iwahara S.-I., Satoh H., Song D.-X., Webb J., Burlingame A.L.,
RA Nagae Y., Muller-Eberhard U.;
RT "Purification, characterization, and cloning of a heme-binding
RL protein (23 kDa) in rat liver cytosol.";
RL Biochemistry 34:13398-13406(1995).
CC
CC -1- FUNCTION: Involved in redox regulation of the cell. Reduces
CC peroxides with reducing equivalents provided through the
CC thioredoxin system but not from glutaredoxin. May play an
CC important role in eliminating peroxides generated during
CC metabolism. Might participate in the signaling cascades of growth
CC factors and tumor necrosis factor-alpha by regulating the
CC intracellular concentrations of H(2)O(2).
CC
CC -1- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By
CC similarity). May form heterodimers with AOP2.
CC
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC
CC -1- MISCELLANEOUS: The active site is the redox-active Cys-52 oxidized
CC to Cys-SOH. Cys-SOH rapidly reacts with Cys-173-SH of the other
CC subunit to form an intermolecular disulfide with a concomitant
CC homodimer formation. The enzyme may be subsequently regenerated by
CC reduction of the disulfide by thioredoxin (By similarity).
CC
CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-
CC 52 (to Cys-SO3H) upon oxidative stress (By similarity).
CC
CC -1- SIMILARITY: BELONGS TO THE AHPc/TSA FAMILY.
CC
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CC
CC
CC DR EMBL; D30035; BAA06275.1; -.
CC DR HSSP; P30041; 1PRX.
CC DR InterPro: IPR000866; AHPc-TSA.
CC DR Pfam: PF00578; AHPc-TSA; 1.
CC KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.
CC FT ACT_SITE 52 52 REDOX-ACTIVE (BY SIMILARITY).
CC FT ACT_SITE 173 173 INTERCHAIN (PARTIAL) (BY SIMILARITY).
CC FT DISULFID 52 173
CC SQ SEQUENCE 199 AA; 22109 MW; BDF2D4AB8A776DA CRC64;
CC
CC Query Match 50.7%; Score 730.5; DB 1; Length 199;
CC Best Local Similarity 70.3%; Pred. No. 1.9e-60;
CC Matches 135; Conservative 24; Mismatches 32; Indels 1; Gaps 1;
CC
CC QY 79 AKISPAPEWEGTAVI-DGEFKELKLDYRGKLVFFFPYLDFTFVCPTEIIAFGRLE 137
CC Db 6 AKIGPAPSFKATAVMPDQGFKDLSYKGYVFFFPYLDFTFVCPTEIIAFGRLE 65
CC
CC QY 138 FRSINTEVAVCSVDSTHLAMINTPRROGGLGPIRIPILSDLRHQISKDYGVLDESGH 197
CC Db 66 FRKLNQVIGASVDSHCHLAWINTSRKSGLSMKIPLVADTRRTISODYGLAKEDEG 125
CC
CC QY 198 HLRGLFTIIDDKGLRQITLNDLPVGRSVDETLRLVQAFQYDKHGEVCPAGKRGSESTI 257
CC Db 126 SFRGLFTIIDDKGLRQITLNDLPVGRSVDETLRLVQAFQYDKHGEVCPAGKRGSESTI 185
CC
CC QY 258 ITPDPAKLYFDK 269
CC Db 186 PDVNSKEYFSK 197
CC
CC RESULT 11
CC PDX1_MOUSE

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ID PDX1_MOUSE STANDARD: PRT: 199 AA.
 AC P35700.
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Peroxiredoxin 1 (EC 1.11.1.-) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2) (Osteoblast specific factor 3) (OSF-3)
 DE (Macrophage 23 kDa stress protein).
 GN PRDX1 OR TDPX2 OR MSP23 OR PACA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC MGI:TaxID=10090.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peritoneal macrophage;
 RX MEDLINE=9336671; PubMed=8360158;
 RA Ishii T., Yamada M., Sato H., Matsue M., Taketani S., Nakayama K., Sugita Y., Bannai S.;
 RT "Cloning and characterization of a 23-kDa stress-induced mouse peritoneal macrophage protein.";
 RL J. Biol. Chem. 268:18633-18636(1993).
 RP [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Osteoblast;
 RX MEDLINE=94375405; PubMed=8089076;
 RA Kawai S., Takeshita S., Okazaki M., Kikuno R., Kudo A., Amann E.;
 RT "Cloning and characterization of OSF-3, a new member of the MERS family, expressed in mouse osteoblastic cells.";
 RL J. Biochem. 115:641-643(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ; TISSUE=Liver;
 RA Hino K., Sato H., Bannai S.;
 RT "Characterization of mouse type I peroxiredoxin gene and pseudogenes.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Involved in redox regulation of the cell. Reduces peroxides with reducing equivalents provided through the thioredoxin system but not from glutaredoxin. May play an important role in eliminating peroxides generated during metabolism. Might participate in the signaling cascades of growth factors and tumor necrosis factor-alpha by regulating the intracellular concentrations of H(2)O(2).
 CC -1- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By similarity). May form heterodimers with AOP2.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: FOUND IN VARIOUS TISSUES: HIGH CONCENTRATION IN LIVER.
 CC -1- INDUCTION: BY OXIDATIVE AND SULFHYDRYL-REACTIVE AGENTS.
 CC -1- MISCELLANEOUS: The active site is the redox-active Cys-52 oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-173-SH of the other subunit to form an intermolecular disulfide with a concomitant homodimer formation. The enzyme may be subsequently regenerated by reduction of the disulfide by thioredoxin (By similarity).
 CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-52 (to Cys-SO3) upon oxidative stress (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE AHPc/TSA FAMILY.
 CC -----
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 CC -----
 DR EMBL: D16142; BAA03713.1; -
 DR EMBL: D21252; BAA04796.1; -
 DR EMBL: AB023564; BAA86992.1; -
 DR EMBL: AB023560; BAA86992.1; JOINED.
 DR EMBL: AB023561; BAA86992.1; JOINED.
 DR EMBL: AB023562; BAA86992.1; JOINED.

DR EMBL: AB023563; BAA86992.1; JOINED.
 DR PIR: A48513; A48513.
 DR PIR: JC2259; JC2259.
 DR HSSP: P30041; 1PRX.
 DR SWISS-2DPAGE: P35700; MOUSE.
 DR MGI:99523; Prdx1.
 DR InterPro: IPR000866; AhpC-TSA.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 DR Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.
 FT ACT SITE 52
 FT DISULFID 52 173 INTERCHAIN (PARTIAL) (BY SIMILARITY).
 SO SEQUENCE 199 AA; 22176 MW; BEF5C995A86124D1 CRC64;
 Query Match 50.1%; Score 721.5; DB 1; Length 199;
 Best Local Similarity 68.8%; Pred. No. 1.3e-59;
 Matches 132; Conservative 27; Mismatches 32; Indels 1; Gaps 1;
 QY 79 AKISKPAVYMEGTAVI-DGEKELKLDYRGKRYLVEFFYPPLDFTFVCPTEIIAFGRLEE 137
 DB 6 AKIGYPAVNFKATVMPDQGFKDLSLEYKGYVFFFPYPLDFTFVCPTEIIAFSDRADE 65
 QY 138 FRSINTEVYACSVDSQFHLAMINPRROGGLGPIRPLSDLRHOSKQGVYLEDSCGH 197
 DB 66 FKLLNCOVIGASVDSHFECHLAMINTPKRQGLGPNINPLISDPKRTIAQDYGVLAKADEGI 125
 QY 198 TLRGLEFIIDKGIIRQLITLNDLPYGRSVDETLRLVQAFQYTDKKGECVPAKMGKPGSETII 257
 DB : |||||FIIDKGIIRQLITLNDLPYGRSVDETLRLVQAFQYTDKKGECVPAKMGKPGSETII 185
 QY 126 SFRGFIIDKGIIRQLITLNDLPYGRSVDETLRLVQAFQYTDKKGECVPAKMGKPGSETII 185
 QY 258 PDPAKGLKYEFDK 269
 DB 186 PDVAKSKYEFSK 197
 RESULT 12
 ID PDX3_HUMAN STANDARD: PRT: 256 AA.
 AC P30048; P35690; Q13776; Q96HK4;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Thioredoxin-dependent peroxide reductase, mitochondrial precursor (EC 1.11.1.-) (Peroxiredoxin 3) (Antioxidant protein 1) (AOP-1) (MERS protein homolog) (HBC189) (PRX III).
 GN PRDX3 OR AOP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NC MGI:TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=95251598; PubMed=7733872;
 RA Tsuji K., Copeland N.G., Jenkins N.A., Obinata M.;
 RT "Mammalian antioxidant protein complements alkyldihydroperoxide reductase (ahpc) mutation in Escherichia coli.";
 RL Biochem. J. 307:377-381(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin, Testis, Urinary bladder, and Uterus;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 148-240 FROM N.A.
 RX MEDLINE=94108427; PubMed=7506601;
 RA Takeda J., Yano H., Eng S., Zeng Y., Bell G.I.;
 RT "A molecular inventory of human pancreatic islets: sequence analysis of 1000 cDNA clones.";
 RL Hum. Mol. Genet. 2:1793-1798(1993).
 RN [4]
 RP SEQUENCE OF 63-72.
 RC TISSUE=Liver;
 RX MEDLINE=93162045; PubMed=1286669;

RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
RA Appel R.D., Hughes G.J.:
RT "Human liver protein map: a reference database established by
RT microsequencing and gel comparison."
RL Electrophoresis 13:992-1001(1992).
RN [5]
RP OXEROXYDATION OF CYS-108.
RA Rabilloud T.:
RL unpublished observations (JUL-2002).
CC -1- FUNCTION: Involved in redox regulation of the cell. Protects
CC radical-sensitive enzymes from oxidative damage by a radical-
CC generating system.
CC -1- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (by
CC similarity).
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- MISCELLANEOUS: The active site is the redox-active Cys-108
CC oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-229-SH of the
CC other subunit to form an intermolecular disulfide with a
CC concomitant homodimer formation. The enzyme may be subsequently
CC regenerated by reduction of the disulfide by thioredoxin.
CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-
CC 108 (to Cys-SO₃H) upon oxidative stress.
CC -1- SIMILARITY: BELONGS TO THE AHPc/TSA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: DA9396; BAA08389.1; -;
DR EMBL: BC002685; AAH02685.1; -;
DR EMBL: BC008038; AAH08038.1; -;
DR EMBL: BC008435; AAH08435.1; -;
DR EMBL: BC021691; AAH21691.1; -;
DR EMBL: BC022373; AAH22373.1; -;
DR EMBL: T10952; -. NOT_ANNOTATED_CDS.
DR SWISS-2DPAGE: P30048; HUMAN.
DR SlenA-2DPAGE: P30048; -;
DR Genew: HGNC:9354; PRDX3.
DR MIM: 604769; -;
DR InterPro: IPR000866; AhpC-TSA.
DR Pfam: PF00578; AhpC-TSA; 1.
KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center;
KW Mitochondrion; Transit peptide.
FT TRANSIT 1 62 MITOCHONDRION.
FT CHAIN 63 256 THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE.
FT ACT_SITE 108 108 REDOX-ACTIVE.
FT DISULFID 108 229 INTERCHAIN (PARTIAL) (BY SIMILARITY).
FT CONFLICT 31 31 R -> W (IN REF. 2; AAH08435).
SQ SEQUENCE 256 AA; 27692 MW; 8BBE7F5E5BEE9BE CRC64;

Query Match 48.8%; Score 703; DB 1; Length 256;
Best Local Similarity 66.5%; Pred. No. 9,1e-58;
Matches 127; Conservative 26; Mismatches 36; Indels 0; Gaps 0;

DB 245 AASKEFKQVN 255
RESULT 13
PDX3_BOVIN STANDARD; PRT; 257 AA.
AC P35705;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Thioredoxin-dependent peroxide reductase, mitochondrial precursor (EC
DE 1.11.1.-) (Peroxiredoxin 3) (Antioxidant protein 1) (AOP-1) (SP-22
DE protein).
GN PDX3 OR AOP1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal medulla;
RX MEDLINE=97069947; PubMed=8912927;
RA Hirai T., Watabe S., Takimoto K., Yago N., Yamamoto Y., Takahashi S.Y.;
RT "The cDNA sequence encoding bovine SP-22, a new defence system
RT against reactive oxygen species in mitochondria."
RL DNA Seq. 6:239-242(1996).
RN [2]
RP SEQUENCE OF 2-257 FROM N.A.
RC TISSUE=Adrenal medulla;
RX MEDLINE=94375407; PubMed=8089078;
RA Watabe S., Kohno H., Kouyama H., Hirai T., Yago N., Nakazawa T.;
RT "Purification and characterization of a substrate protein for
RT mitochondrial ATP-dependent protease in bovine adrenal cortex."
RL J. Biochem. 115:648-654(1994).
CC -1- FUNCTION: Involved in redox regulation of the cell. Protects
CC radical-sensitive enzymes from oxidative damage by a radical-
CC generating system.
CC -1- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (by
CC similarity).
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- MISCELLANEOUS: The active site is the redox-active Cys-109
CC oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-230-SH of the
CC other subunit to form an intermolecular disulfide with a
CC concomitant homodimer formation. The enzyme may be subsequently
CC regenerated by reduction of the disulfide by thioredoxin (by
CC similarity).
CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-
CC 109 (to Cys-SO₃H) upon oxidative stress (by similarity).
CC -1- SIMILARITY: BELONGS TO THE AHPc/TSA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D82025; BAA1511.1; -;
DR HSP: P30041; IPRX.
DR InterPro: IPR000866; AhpC-TSA.
DR Pfam: PF00578; AhpC-TSA; 1.
KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center;
KW Mitochondrion; Transit peptide.
FT TRANSIT 1 63 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 64 257 THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE.
FT ACT_SITE 109 109 REDOX-ACTIVE (BY SIMILARITY).
FT DISULFID 109 230 INTERCHAIN (PARTIAL) (BY SIMILARITY).
SQ SEQUENCE 257 AA; 28195 MW; F2E89EE2F172A42D CRC64;

Query Match 48.0%; Score 691; DB 1; Length 257;
Best Local Similarity 65.4%; Pred. No. 1.2e-56;

Matches 125; Conservative 28; Mismatches 38; Indels 0; Gaps 0;

QY 81 ISKPAWMEGTAVIDGEEFKELTDYRGKYLVFFYPPLDFTVCPEITIAFGRLSEFRS 140
 Db 66 VTQHAHYFEGTAVVGESEFKELSLDDEKFKYLVFFYPPLDFTVCPEITIAFGRLSEFRS 125

QY 141 INTEVAVACVDSOFTHLAMINTPRROGCGIPRIPLSLDTHQISKDYGVLDSGHTLR 200
 Db 126 VNCVAVAVSDSHFSLAMINTPRKNNGGLGHMIALSLDKQISRDYGVLLSGALALR 185

QY 201 GLEFIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDKHGVCAPGKPGSEITIDP 260
 Db 186 GLEFIIDPNCVIVKHLNVNDLPVGRSVDETLRLVKAQFVETHEGVCAPMWPSPPTIKRSP 245

QY 261 AGKLYFPDKLN 271
 Db 246 TASREYFEKVN 256

RESULT 14
 PD3X_MOUSE STANDARD; PRT: 257 AA.

AC P20108;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Thiorodoxin-dependent peroxidase, mitochondrial precursor (EC 1.11.1.-) (Peroxidoxin 3) (Antioxidant protein 1) (AOP-1) (MERS protein) (PRX III).
 DE PRDX3 OR AOP1 OR MERS.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBL_TaxID=10090;
 RN [1]

RP MEDLINE=90060782; Pubmed=2583515;
 RA Yamamoto T., Matsui Y., Natori S., Obinata M.;
 RT Cloning of a housekeeping-type gene (MERS) preferentially expressed in murine erythroleukemia cells.;
 RL Gene 80:337-343(1989).

CC -1- FUNCTION: Involved in redox regulation of the cell. Protects radical-sensitive enzymes from oxidative damage by a radical-generating system.
 CC -1- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By similarity).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
 CC -1- TISSUE SPECIFICITY: Housekeeping-type gene preferentially expressed in murine erythroleukemia (MEL) cells.
 CC -1- INDUCTION: Expression is increased after induction of MEL cells to differentiation by DMSO.
 CC -1- MISCELLANEOUS: The active site is the redox-active Cys-109 oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-230-SH of the other subunit to form an intermolecular disulfide with a concomitant homodimer formation. The enzyme may be subsequently regenerated by reduction of the disulfide by thiorodoxin (By similarity).
 CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-109 (to Cys-SO₃H) upon oxidative stress (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.

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CC EMBL: M28723; AAA39524.1; -
 CC PIR: J00064; J00064.
 CC MGI: MGI:88034; Prdx3.
 CC InterPro: IPR000866; Ahpc-TSA.

DR Pfam: PF00578; Ahpc-TSA; 1.
 KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center; Mitochondrion; Transil peptide.
 FT TRANSIT 1 63 MITOCHONDRION (BY SIMILARITY).
 FT CHAIN 64 257 THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE.
 FT ACT_SITE 109 109 REDOX-ACTIVE (BY SIMILARITY).
 FT DISULFID 109 230 INTERCHAIN (PARTIAL) (BY SIMILARITY).
 SQ SEQUENCE 257 AA; 28127 MW; 65513F2C5F1D56C0 CRC64;

Query Match 47.8%; Score 689; DB 1; Length 257;
 Best Local Similarity 64.4%; Pred. No. 1.8e-56;
 Matches 123; Conservative 32; Mismatches 36; Indels 0; Gaps 0;

QY 81 ISKPAWMEGTAVIDGEEFKELTDYRGKYLVFFYPPLDFTVCPEITIAFGRLSEFRS 140
 Db 66 VTQHAHYFEGTAVVGESEFKELSLDDEKFKYLVFFYPPLDFTVCPEITIAFGRLSEFRS 125

QY 141 INTEVAVACVDSOFTHLAMINTPRROGCGIPRIPLSLDTHQISKDYGVLDSGHTLR 200
 Db 126 VNCVAVAVSDSHFSLAMINTPRKNNGGLGHMIALSLDKQISRDYGVLLSGALALR 185

QY 201 GLEFIIDDKGILRQITLNDLPVGRSVDETLRLVQAFQYTDKHGVCAPGKPGSEITIDP 260
 Db 186 GLEFIIDPNCVIVKHLNVNDLPVGRSVDETLRLVKAQFVETHEGVCAPMWPSPPTIKRSP 245

QY 261 AGKLYFPDKLN 271
 Db 246 TASREYFEKVN 256

RESULT 15
 TD3X_BRUMA STANDARD; PRT: 199 AA.

AC Q17172;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thiorodoxin peroxidase 2 (Thiorodoxin-dependent peroxidase reductase 2) (thiol-specific antioxidant protein 2).
 OS Brugia malayi.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Brugia.
 NC NCBL_TaxID=6279;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Ghosh I., Raghavan N., Blaxter M., Scott A.L.;
 RL Submitted (FEB-1996) to the EMBL/Genbank/DBJ databases.
 RN [2]

CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED, UPON OXIDATION (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- PTM: THE CYS-53-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY H(2)O(2), AND THE OXIDIZED CYS-53 (PROBABLY CYS-SOH) RAPIDLY REACTS WITH CYS-174-SH OF THE OTHER SUBUNIT TO FORM AN INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE REDUCED BY THIOREDOXIN (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.

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DR EMBL: U47100; AAB67873.1; -.

DR HSP; P30041; IPX.

DR InterPro: IPR000866; Ahpc-TSA.

DR Pfam: PF00578; Ahpc-TSA; 1.

KW Antioxidant.

FT ACT_SITE 53 53

FT ACT_SITE 174 174

SQ SEQUENCE 199 AA; 22042 MW; 8932BD8898B271B CRC64;

Query Match

Best Local Similarity 46.3%; Score 667; DB 1; Length 199;

Matches 123; Conservative 26; Mismatches 44; Indels 0; Gaps 0;

QY 77 SKAKISKPAWEGTAVNIDGFEKELKLTIDYRGKYLVFFFPPLDFTFVCPTEIIAFGDRLE 136
DB 6 SKAFIQPAPNFKTFVAVNGDFKEISLGQFKGYVLLFYPPLDFTFVCPTEIIAFSDRIA 65
QY 137 EFRSINTEVYACSVDSQFTFLAMINTPRQGGIGPIRIPPLSDLNQISKDYGVLLEDG 196
DB 66 EFKOLDVAVMACSTDSEHFSHLAMVNTDRKMGIGQMNPILAYTNHVISRAVGLKEDDG 125
QY 197 HTLRGLFIIDDKGILBQITLNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGMKPGSETI 256
DB 126 IAYRGLEFIIDPKGILQITINDLPVGRSVDETLRLVQAFQYVDKHGEVCPANMHPGSETI 185
QY 257 IPPPAGKLYFDK 269
DB 186 KPGVKESKAYFEK 198

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